Sequence Alignment

PR 01-APR-1998; 98US-0080333P.
PR 01-APR-1998; 98US-0080334P.
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PR 09-APR-1998; 98US-0081203P.
PR 09-APR-1998; 98US-0081229P.
PR 15-APR-1998; 98US-0081817P.
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PR 22-APR-1998; 98US-0082700P.
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PR 23-APR-1998; 98US-0082767P.
PR 23-APR-1998; 98US-0082796P.
PR 27-APR-1998; 98US-0083336P.
PR 28-APR-1998; 98US-0083322P.
PR 29-APR-1998; 98US-0083392P.
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PR 29-APR-1998; 98US-0083496P.
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PR 29-APR-1998; 98US-0083500P.
PR 29-APR-1998; 98US-0083545P.
PR 29-APR-1998; 98US-0083554P.
PR 29-APR-1998; 98US-0083558P.
PR 29-APR-1998; 98US-0083559P.
PR 30-APR-1998; 98US-0083742P.
PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 06-MAY-1998; 98US-0084441P.
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PR 07-MAY-1998; 98US-0084600P.
PR 07-MAY-1998; 98US-0084627P.
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PR 13-MAY-1998; 98US-0085339P.
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PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085689P.
PR 15-MAY-1998; 98US-0085697P.
PR 15-MAY-1998; 98US-0085700P.
PR 15-MAY-1998; 98US-0085704P.
PR 18-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086392P.
PR 22-MAY-1998; 98US-0086414P.
PR 22-MAY-1998; 98US-0086430P.
PR 22-MAY-1998; 98US-0086486P.
PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087106P.
PR 28-MAY-1998; 98US-0087208P.
PR 30-JUL-1998; 98US-0094651P.
PR 11-SEP-1998; 98US-0100038P.
XX
PA (GETH) GENENTECH INC.
XX
PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX
DR WPI; 1999-551358/46.
DR N-PSDB; AAZ34205.
XX
PT New secreted and transmembrane polypeptides and their polynucleotides,
PT useful for treating blood coagulation disorders, cancers and cellular
PT adhesion disorders.
XX
PS Claim 12; Fig 149; 530pp; English.
XX
CC The present invention describes secreted and transmembrane polypeptides
CC and their polynucleotides. The nucleotide sequences are useful as sources
CC of probes, primers, for chromosome mapping, and for generation of
CC antisense sequences. They can also be used to create transgenic animals.
CC The proteins can be used to treat a variety of diseases and disorders,
CC depending on their function. Diseases that may be treated include blood
CC coagulation disorders, cancers and cellular adhesion disorders. They may
CC also be used to raise antibodies. AAZ33891 to AAZ34338, and AAY41685 to
CC AAY41774 represent polynucleotide and polypeptide sequence given in the
CC exemplification of the present invention
XX
SQ Sequence 111 AA;

Query Match 100.0%; Score 587; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 8.9e-60;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60
Db 1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60

Qy 61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
Db 61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111

RESULT 2
AAY28290
ID AAY28290 standard; protein; 111 AA.
XX
AC AAY28290;
XX
DT 28-SEP-1999 (first entry)
XX
DE Tim-1 protein.
XX
KW Chemokine; CXC; Tim-1; inflammation; heart attack; stroke; infection; ss;
KW trauma; radiation; burns; frostbite; corrosive chemical; gene therapy.
XX
OS Homo sapiens.
XX
PN WO9933990-A1.
XX
PD 08-JUL-1999.
XX
PF 14-DEC-1998; 98WO-US026546.
XX
PR 30-DEC-1997; 97US-0068955P.
XX
PA (CHIR) CHIRON CORP.
XX
PI Chen TT, Pot D, Kassam A;
XX
DR WPI; 1999-430244/36.
DR N-PSDB; AAX89708.
XX
PT A new human CXC chemokine, Tim-1, useful for treating inflammation.
XX
PS Claim 1; Page 43; 46pp; English.
XX
CC This is the amino acid sequence for the Tim-1 CXC chemokine. The Tim-1
CC gene can be used to design therapeutic tools for treating inflammation
CC due to stimuli such as heart attacks and stroke, infection, physical
CC trauma, UV or ionizing radiation, burns, frostbite or corrosive
CC chemicals. The Tim-1 gene and subgenomic polynucleotides can be used in
CC gene therapy
XX
SQ Sequence 111 AA;

Query Match 100.0%; Score 587; DB 2; Length 111;

```
 Best Local Similarity   100.0%;  Pred. No. 8.9e-60;
 Matches  111;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60

Qy         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111


RESULT 3
AAB33423
ID   AAB33423 standard; protein; 111 AA.
XX
AC   AAB33423;
XX
DT   29-JAN-2001  (first entry)
XX
DE   Human PRO273 protein UNQ240 SEQ ID NO:46.
XX
KW   Human; immune related disease; diagnosis; antiinflammatory; cardiant;
KW   dermatological; antiarthritic; antirheumatic; immunosuppressive;
KW   haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
KW   antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;
KW   antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
KW   osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
KW   idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
KW   systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
KW   autoimmune thrombocytopaenia; immune-mediated renal disease;
KW   demyelinating disease; hepatobiliary disease; Whipple's disease;
KW   inflammatory bowel disease; gluten-sensitive enteropathy;
KW   autoimmune disease; immune-mediated skin disease; allergic disease;
KW   immunological disease; transplantation associated disease;
KW   graft rejection; graft-versus-host-disease.
XX
OS   Homo sapiens.
XX
PN   WO200053758-A2.
XX
PD   14-SEP-2000.
XX
PF   02-MAR-2000; 2000WO-US005841.
XX
PR   08-MAR-1999;   99WO-US005028.
PR   10-MAR-1999;   99US-0123618P.
PR   12-MAR-1999;   99US-0123957P.
PR   23-MAR-1999;   99US-0125775P.
PR   12-APR-1999;   99US-0128849P.
PR   20-APR-1999;   99WO-US008615.
PR   28-APR-1999;   99US-0131445P.
PR   04-MAY-1999;   99US-0132371P.
PR   14-MAY-1999;   99US-0134287P.
PR   02-JUN-1999;   99WO-US012252.
PR   23-JUN-1999;   99US-0141037P.
PR   20-JUL-1999;   99US-0144758P.
PR   26-JUL-1999;   99US-0145698P.
PR   28-JUL-1999;   99US-0146222P.
PR   01-SEP-1999;   99WO-US020111.
PR   08-SEP-1999;   99WO-US020594.
PR   13-SEP-1999;   99WO-US020944.
PR   15-SEP-1999;   99WO-US021090.
PR   15-SEP-1999;   99WO-US021547.
PR   05-OCT-1999;   99WO-US023089.
PR   29-OCT-1999;   99US-0162506P.
PR   29-NOV-1999;   99WO-US028214.
PR   30-NOV-1999;   99WO-US028313.
PR   30-NOV-1999;   99WO-US028409.
PR   01-DEC-1999;   99WO-US028301.
PR   01-DEC-1999;   99WO-US028634.
PR   02-DEC-1999;   99WO-US028551.
PR   02-DEC-1999;   99WO-US028564.
PR   02-DEC-1999;   99WO-US028565.
PR   16-DEC-1999;   99WO-US030095.
PR   20-DEC-1999;   99WO-US030999.
PR   30-DEC-1999;   99WO-US031274.
PR   05-JAN-2000; 2000WO-US000219.
PR   06-JAN-2000; 2000WO-US000277.
PR   06-JAN-2000; 2000WO-US000376.
PR   11-FEB-2000; 2000WO-US003565.
PR   18-FEB-2000; 2000WO-US004341.
PR   18-FEB-2000; 2000WO-US004342.
PR   22-FEB-2000; 2000WO-US004414.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Goddard A,  Gurney AL,  Hebert C,  Henzel W;
PI   Kabakoff RC,  Lu Y,  Pan J,  Pennica D,  Shelton DL,  Smith V;
PI   Stewart TA,  Tumas D,  Watanabe CK,  Wood WI,  Yan M;
XX
DR   WPI; 2000-572271/53.
DR   N-PSDB; AAC58588.
XX
PT   Sixty four PRO polypeptides, useful in the diagnosis and treatment of
PT   immune related disorders, e.g. systemic lupus erythematosis, rheumatoid
PT   arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
XX
PS   Claim 33; Fig 20; 309pp; English.
XX
CC   The present invention describes sixty four human PRO proteins which can
CC   be used in the treatment of immune related diseases. The human PRO
CC   proteins, anti-PRO antibodies, agonists and antagonists are useful for
CC   treating and diagnosing immune related disorders. The disorders are
CC   selected from systemic lupus erythematosus, rheumatoid arthritis,
CC   osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
CC   systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC   syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
CC   anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
CC   immune-mediated renal disease, demyelinating diseases of the central and
CC   peripheral nervous systems, hepatobiliary diseases, inflammatory bowel
CC   disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune
CC   or immune-mediated skin diseases, allergic diseases, immunological
CC   diseases of the lung, and transplantation associated diseases including
CC   graft rejection and graft-versus-host-disease. AAC58397 to AAC58578
CC   represent PCR primers and hybridisation probes used in the isolation of
CC   human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477
CC   represent human PRO polynucleotide and protein sequences given in the
CC   exemplification of the present invention
XX
SQ   Sequence 111 AA;

  Query Match           100.0%;  Score 587;  DB 3;  Length 111;
  Best Local Similarity  100.0%;  Pred. No. 8.9e-60;
  Matches  111;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60

Qy         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111


RESULT 4
AAB44295
ID   AAB44295 standard; protein; 111 AA.
XX
AC   AAB44295;
XX
DT   08-FEB-2001  (first entry)
XX
DE   Human PRO273 (UNQ240) protein sequence SEQ ID NO:370.
XX
KW   Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;
```

```
;  CURRENT FILING DATE:  1999-05-14
;  NUMBER OF SEQ ID NOS: 425
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 263
;   LENGTH: 764
;   TYPE: DNA
;   ORGANISM: Mouse
US-09-312-283C-263

  Query Match             26.6%;  Score 448;  DB 4;  Length 764;
  Best Local Similarity   79.7%;  Pred. No. 7.6e-96;
  Matches  606;  Conservative    0;  Mismatches  115;  Indels   39;  Gaps    5;

Qy          11 GCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGGCGCAGCCGGA 70
               ||  || || |   |||| || |||||| | |  | ||| ||| ||||||     | |||
Db          13 GCCAAGCGCACCAGGCACCGCGACAGAC-GGCAGGAGCACCCATCGACGGGCGTACTGGA 71

Qy          71 GCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCTGGGTGGCGTC 130
               || ||| |||| |    | | |   || ||    ||    || |  ||| ||| ||| ||
Db          72 GCGAGCCGAGCAGAGCAGAGAGAGGCGTGCTTGAAACCGAGAACCAAGCCGGGCGGCATC 131

Qy         131 TCCGGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCCACGCCGCGCC 190
               || |||||||| |  || |||| ||||||||     |||||||||| | |||||||
Db         132 CCCCGGCCGCCGCACGCACAGGCCGGCGCCCTCCTTGCCTCCCTGCTCCC-CACCGCGCC 190

Qy         191 CCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCTGGCGCTGTAC 250
               ||||||| |||||||||||||||||||||||||||||||||||||||| |||||||||| |
Db         191 CCTCCGGCCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTCCTGGCGCTGTGC 250

Qy         251 ACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAAGATCCGCTAC 310
               || |||| |||||||||||||| || ||||| ||||||||||| ||||||||||||||||
Db         251 GCCTCGCGCGTGGACGGGTCCAAGTGTAAGTGTTCCCGGAAGGGGCCCAAGATCCGCTAC 310

Qy         311 AGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGAGAAGATGGTT 370
               |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db         311 AGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCACACTGCGAGGAGAAGATGGTT 370

Qy         371 ATCATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCTGCACCCCAAG 430
               ||| |||||||||||||| |||||||||||||| || |||||||||||||||||||| |||
Db         371 ATCGTCACCACCAAGAGCATGTCCAGGTACCGGGGCCAGGAGCACTGCCTGCACCCTAAG 430

Qy         431 CTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAAGCGCAGGGTC 490
               ||||||||||||||| ||||||||||||||||||||| |||||||||||||||||||||||
Db         431 CTGCAGAGCACCAAACGCTTCATCAAGTGGTACAATGCCTGGAACGAGAAGCGCAGGGTC 490

Qy         491 TACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTGGGAGACTTGT 550
               |||||||||||||||| |  | |   ||| | |||||||||  ||||||| |||||||
Db         491 TACGAAGAATAGGGTGGACGATCATGGAAAGAAAAACTCCAGGCCAGTTGAGAGACTTCA 550

Qy         551 GCAAAGGACTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 610
               ||| ||||||||||||||                                  |||| ||
Db         551 GCAGAGGACTTTGCAGATT---------------------------------AAAATAA 576

Qy         611 AAAGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGAAGCACTTTTT 670
               ||  |||||||||||||| |||||||  |||||||||||||| |||||||| ||| ||
Db         577 AAGCCCTTTCTTTCTCACAAGCATAAG--ACAAATTATATATTGCTATGAAGCTCTTCTT 634

Qy         671 ACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGATGGGAGACCC 730
               ||| | |||||||||||||||||||||||| ||| ||||||||||||||| |||| ||
Db         635 ACC-AGGGTCAGTTTTTACATTTTATAGCTGTGTGTGAAAGGCTTCCAGATGTGAGATCC 693

Qy         731 ATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTT 770
               | ||| | || || |||||||||||| ||| |  |||||||
Db         694 AGCTCGCCTGCGCACCAGACTTCATTACAAGTGGCTTTTT 733


RESULT 10
US-08-825-556A-1
; Sequence 1, Application US/08825556A
; Patent No. 5910431
;  GENERAL INFORMATION:
;    APPLICANT:  Ni, Jian
;    APPLICANT:  Gentz, Reiner L.
;    APPLICANT:  Su, Jeffrey Y.
;    APPLICANT:  Li, Haodong
;    TITLE OF INVENTION:  Chemokine Alpha 2
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox, P.L.L.C.
;      STREET:  1100 New York Ave., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-2934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/825,556A
;      FILING DATE:  19-MAR-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/013,653
;      FILING DATE:  19-MAR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steffe, Eric K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.0850001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  461 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  both
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  43..375
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  79..375
;    FEATURE:
;      NAME/KEY:  sig_peptide
;      LOCATION:  43..126
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  127..375
;    FEATURE:
;      NAME/KEY:  sig_peptide
;      LOCATION:  79..126
US-08-825-556A-1

  Query Match             25.9%;  Score 435.6;  DB 2;  Length 461;
  Best Local Similarity   98.7%;  Pred. No. 4.9e-93;
  Matches  450;  Conservative    0;  Mismatches    4;  Indels    2;  Gaps    1;

Qy         130 CTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCCACGCCGCGC 189
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           6 CTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCCACGCCGCGC 65

Qy         190 CCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCTGGCGCTGTA 249
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          66 CCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCTGGCGCTGTA 125

Qy         250 CACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAAGATCCGCTA 309
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         126 CACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAAGATCCGCTA 185

Qy         310 CAGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGAGAAGATGGT 369
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         186 CAGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGAGAAGATGGT 245
```

```
Qy        370 TATCATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCTGCACCCCAA 429
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 TATCATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCTGCACCCCAA 305

Qy        430 GCTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAAGCGCAGGGT 489
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        306 GCTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAAGCGCAGGTT 365

Qy        490 CTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTGGGAGACTTG 549
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 CTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTGGGAGACTTG 425

Qy        550 TG--CAAAGGACTTTGCAGATTAAAAAAAAAAAAAA 583
              ||  || | ||||||||||||||||||||||||||||
Db        426 TGGCAAAGGAACTTTGCAGATTAAAAAAAAAAAAAA 461


RESULT 11
US-09-238-184-1
; Sequence 1, Application US/09238184
; Patent No. 6479633
;  GENERAL INFORMATION:
;    APPLICANT:  Ni, Jian
;    APPLICANT:  Gentz, Reiner L.
;    APPLICANT:  Su, Jeffrey Y.
;    APPLICANT:  Li, Haodong
;    TITLE OF INVENTION:  Chemokine Alpha 2
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox, P.L.L.C.
;      STREET:  1100 New York Ave., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-2934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/238,184
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/825,556
;      FILING DATE:  19-MAR-1997
;      APPLICATION NUMBER:  US 60/013,653
;      FILING DATE:  19-MAR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steffe, Eric K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.0850001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  461 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  both
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  43..375
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  79..375
;    FEATURE:
;      NAME/KEY:  sig_peptide
;      LOCATION:  43..126
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  127..375
;    FEATURE:
;      NAME/KEY:  sig_peptide
;      LOCATION:  79..126
US-09-238-184-1

  Query Match             25.9%;  Score 435.6;  DB 4;  Length 461;
  Best Local Similarity   98.7%;  Pred. No. 4.9e-93;
  Matches  450;  Conservative    0;  Mismatches    4;  Indels    2;  Gaps    1;

Qy        130 CTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCCACGCCGCGC 189
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 CTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCCACGCCGCGC 65

Qy        190 CCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCTGGCGCTGTA 249
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 CCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCTGGCGCTGTA 125

Qy        250 CACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAAGATCCGCTA 309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 CACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAAGATCCGCTA 185

Qy        310 CAGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGAGAAGATGGT 369
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CAGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGAGAAGATGGT 245

Qy        370 TATCATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCTGCACCCCAA 429
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 TATCATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCTGCACCCCAA 305

Qy        430 GCTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAAGCGCAGGGT 489
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        306 GCTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAAGCGCAGGTT 365

Qy        490 CTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTGGGAGACTTG 549
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 CTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTGGGAGACTTG 425

Qy        550 TG--CAAAGGACTTTGCAGATTAAAAAAAAAAAAAA 583
              ||  || | ||||||||||||||||||||||||||||
Db        426 TGGCAAAGGAACTTTGCAGATTAAAAAAAAAAAAAA 461


RESULT 12
US-09-188-930-38
; Sequence 38, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
;  APPLICANT: Watson, James D.
;  APPLICANT: Strachan, Lorna
;  APPLICANT: Sleeman, Matthew
;  APPLICANT: Onrust, Rene
;  APPLICANT: Murison, James Greg
;  TITLE OF INVENTION: Compositions Isolated From Skin Cells
;  TITLE OF INVENTION: and Methods For Their Use
;  FILE REFERENCE: 11000.1011c1
;  CURRENT APPLICATION NUMBER: US/09/188,930A
;  CURRENT FILING DATE: 1998-11-09
;  NUMBER OF SEQ ID NOS: 348
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 38
;   LENGTH: 766
;   TYPE: DNA
;   ORGANISM: mouse
US-09-188-930-38

  Query Match             25.3%;  Score 426;  DB 3;  Length 766;
  Best Local Similarity   79.5%;  Pred. No. 1.1e-90;
  Matches  606;  Conservative    0;  Mismatches  115;  Indels   41;  Gaps    7;

Qy         11 GCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGGCGCAGCCGGA 70
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 22, 2004, 12:31:18 ; Search time 22 Seconds
(without alignments)
260.476 Million cell updates/sec

Title: US-09-978-189-370
Perfect score: 587
Sequence: 1 MSLLPRRAPPVSMRLLAAAL.....TKRFIKWYNAWNEKRRVYEE 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	582	99.1	111	2	US-08-825-556A-2	Sequence 2, Appli
2	582	99.1	111	4	US-09-238-184-2	Sequence 2, Appli
3	522	88.9	99	2	US-08-825-556A-3	Sequence 3, Appli
4	522	88.9	99	4	US-09-238-184-3	Sequence 3, Appli
5	509	86.7	95	3	US-09-188-930-344	Sequence 344, App
6	509	86.7	95	4	US-09-724-864-68	Sequence 68, Appl
7	509	86.7	95	4	US-09-312-283C-344	Sequence 344, App
8	506	86.2	99	3	US-09-188-930-340	Sequence 340, App
9	506	86.2	99	4	US-09-312-283C-340	Sequence 340, App
10	506	86.2	99	4	US-09-312-283C-394	Sequence 394, App
11	506	86.2	99	4	US-09-312-283C-417	Sequence 417, App
12	504.5	85.9	98	4	US-09-312-283C-418	Sequence 418, App
13	428	72.9	77	3	US-09-188-930-346	Sequence 346, App
14	428	72.9	77	4	US-09-724-864-72	Sequence 72, Appl
15	428	72.9	77	4	US-09-312-283C-346	Sequence 346, App
16	424	72.2	77	3	US-09-188-930-345	Sequence 345, App
17	424	72.2	77	4	US-09-724-864-70	Sequence 70, Appl
18	424	72.2	77	4	US-09-312-283C-345	Sequence 345, App
19	414	70.5	75	4	US-09-177-304-3	Sequence 3, Appli
20	298	50.8	133	3	US-09-188-930-157	Sequence 157, App
21	298	50.8	133	4	US-09-312-283C-157	Sequence 157, App
22	143.5	24.4	98	2	US-08-825-556A-4	Sequence 4, Appli
23	143.5	24.4	98	4	US-09-238-184-4	Sequence 4, Appli
24	143.5	24.4	100	4	US-08-679-493A-146	Sequence 146, App
25	138	23.5	100	3	US-08-476-376-2	Sequence 2, Appli
26	138	23.5	100	4	US-09-312-283C-423	Sequence 423, App
27	128.5	21.9	107	1	US-08-352-324A-4	Sequence 4, Appli
28	128.5	21.9	107	2	US-08-862-607-4	Sequence 4, Appli
29	128.5	21.9	107	2	US-08-468-819-6	Sequence 6, Appli
30	128.5	21.9	107	3	US-09-203-235-4	Sequence 4, Appli
31	128.5	21.9	107	4	US-09-213-383-6	Sequence 6, Appli
32	128.5	21.9	107	5	PCT-US95-16144-4	Sequence 4, Appli
33	117.5	20.0	107	1	US-08-352-324A-7	Sequence 7, Appli
34	117.5	20.0	107	2	US-08-862-607-7	Sequence 7, Appli
35	117.5	20.0	107	2	US-08-468-819-5	Sequence 5, Appli
36	117.5	20.0	107	3	US-09-203-235-7	Sequence 7, Appli
37	117.5	20.0	107	4	US-09-213-383-5	Sequence 5, Appli
38	117.5	20.0	107	5	PCT-US95-16144-7	Sequence 7, Appli
39	113	19.3	71	2	US-08-812-003-9	Sequence 9, Appli
40	111	18.9	96	4	US-08-649-006A-7	Sequence 7, Appli
41	111	18.9	96	4	US-09-771-023-9	Sequence 9, Appli
42	111	18.9	96	4	US-09-312-283C-424	Sequence 424, App
43	109	18.6	106	4	US-08-679-493A-148	Sequence 148, App
44	107	18.2	106	1	US-08-352-324A-5	Sequence 5, Appli
45	107	18.2	106	2	US-08-862-607-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-08-825-556A-2
; Sequence 2, Application US/08825556A
; Patent No. 5910431
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Su, Jeffrey Y.
; APPLICANT: Li, Haodong
; TITLE OF INVENTION: Chemokine Alpha 2
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-2934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/825,556A
; FILING DATE: 19-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,653
; FILING DATE: 19-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0850001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-825-556A-2

Query Match 99.1%; Score 582; DB 2; Length 111;
Best Local Similarity 99.1%; Pred. No. 1.4e-63;
Matches 110; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60

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                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60

Qy         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
                  |||||||||||||||||||||||||||||||||||||||||||||||| |||
Db         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRFYEE 111


RESULT 2
US-09-238-184-2
; Sequence 2, Application US/09238184
; Patent No. 6479633
;  GENERAL INFORMATION:
;    APPLICANT:  Ni, Jian
;    APPLICANT:  Gentz, Reiner L.
;    APPLICANT:  Su, Jeffrey Y.
;    APPLICANT:  Li, Haodong
;    TITLE OF INVENTION:  Chemokine Alpha 2
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox, P.L.L.C.
;      STREET:  1100 New York Ave., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-2934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/238,184
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/825,556
;      FILING DATE:  19-MAR-1997
;      APPLICATION NUMBER:  US 60/013,653
;      FILING DATE:  19-MAR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steffe, Eric K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.0850001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  111 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-238-184-2

  Query Match             99.1%;  Score 582;  DB 4;  Length 111;
  Best Local Similarity   99.1%;  Pred. No. 1.4e-63;
  Matches  110;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60

Qy         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
              ||||||||||||||||||||||||||||||||||||||||||||||| |||
Db         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRFYEE 111


RESULT 3
US-08-825-556A-3
; Sequence 3, Application US/08825556A
; Patent No. 5910431
;  GENERAL INFORMATION:
;    APPLICANT:  Ni, Jian
;    APPLICANT:  Gentz, Reiner L.
;    APPLICANT:  Su, Jeffrey Y.
;    APPLICANT:  Li, Haodong
;    TITLE OF INVENTION:  Chemokine Alpha 2
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox, P.L.L.C.
;      STREET:  1100 New York Ave., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-2934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/825,556A
;      FILING DATE:  19-MAR-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/013,653
;      FILING DATE:  19-MAR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steffe, Eric K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.0850001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  99 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-825-556A-3

  Query Match             88.9%;  Score 522;  DB 2;  Length 99;
  Best Local Similarity   99.0%;  Pred. No. 2.6e-56;
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Qy         13 MRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIITT 72
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Db          1 MRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIITT 60

Qy         73 KSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
              ||||||||||||||||||||||||||||||||||||||| |||
Db         61 KSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRFYEE 99


RESULT 4
US-09-238-184-3
; Sequence 3, Application US/09238184
; Patent No. 6479633
;  GENERAL INFORMATION:
;    APPLICANT:  Ni, Jian
;    APPLICANT:  Gentz, Reiner L.
;    APPLICANT:  Su, Jeffrey Y.
;    APPLICANT:  Li, Haodong
;    TITLE OF INVENTION:  Chemokine Alpha 2
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox, P.L.L.C.
;      STREET:  1100 New York Ave., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-2934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
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GenCore version 5.1.6

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Run on: April 22, 2004, 12:29:47 ; Search time 40 Seconds
(without alignments)
875.563 Million cell updates/sec

Title: US-09-978-189-370
Perfect score: 587
Sequence: 1 MSLLPRRAPPVSMRLLAAAL.....TKRFIKWYNAWNEKRRVYEE 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
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7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	582	99.1	111	4	Q9NS21	Q9ns21 homo sapien
2	507	86.4	99	11	Q8K453	Q8k453 rattus norv
3	506	86.2	99	11	Q9JHH7	Q9jhh7 mus musculu
4	488	83.1	95	11	Q91V02	Q91v02 mus musculu
5	335	57.1	100	13	Q9DFG4	Q9dfg4 brachydanio
6	322.5	54.9	98	13	Q9DGL8	Q9dgl8 gallus gall
7	143.5	24.4	101	11	Q9EP62	Q9ep62 rattus norv
8	128.5	21.9	108	6	Q28724	Q28724 oryctolagus
9	128	21.8	100	11	Q91ZK9	Q91zk9 sigmodon hi
10	126.5	21.6	101	11	Q91Z64	Q91z64 sigmodon hi
11	121.5	20.7	107	6	Q8HXZ4	Q8hxz4 macaca mula
12	119.5	20.4	107	6	Q8HXZ3	Q8hxz3 macaca mula
13	100	17.0	95	13	Q7T0B3	Q7t0b3 ictalurus p
14	97.5	16.6	97	13	Q98TQ2	Q98tq2 oncorhynchu
15	94.5	16.1	97	13	Q7SX73	Q7sx73 oncorhynchu
16	94.5	16.1	113	6	Q8MIN2	Q8min2 equus cabal
17	93.5	15.9	126	11	Q99J60	Q99j60 mus musculu
18	89.5	15.2	97	13	Q8QFP5	Q8qfp5 cyprinus ca
19	89.5	15.2	100	13	Q8AXP4	Q8axp4 chimaera ph
20	89.5	15.2	126	11	Q8C9J0	Q8c9j0 mus musculu
21	89	15.2	95	13	Q7T0B4	Q7t0b4 ictalurus p
22	89	15.2	113	11	Q9EQI5	Q9eqi5 mus musculu
23	88	15.0	95	13	Q7T0B2	Q7t0b2 ictalurus f
24	88	15.0	109	13	Q90Y59	Q90y59 paralichthy
25	87.5	14.9	111	11	Q99ME0	Q99me0 rattus norv
26	87	14.8	98	13	Q8QGV8	Q8qgv8 paralichthy
27	86.5	14.7	104	13	O73912	O73912 gallus gall
28	86	14.7	93	13	Q9PTF8	Q9ptf8 brachydanio
29	84.5	14.4	116	11	Q91ZB2	Q91zb2 mus musculu
30	84.5	14.4	117	11	Q8C9B8	Q8c9b8 mus musculu
31	83.5	14.2	102	6	Q95MZ7	Q95mz7 ovis aries
32	83.5	14.2	102	6	Q867B3	Q867b3 capra hircu
33	83.5	14.2	117	12	Q68398	Q68398 human cytom
34	83	14.1	94	6	Q8MIZ0	Q8miz0 macaca mula
35	81.5	13.9	101	13	Q8UW91	Q8uw91 triakis scy
36	80.5	13.7	98	6	Q8MIZ1	Q8miz1 macaca mula
37	80.5	13.7	98	6	Q865F5	Q865f5 macaca neme
38	79.5	13.5	101	6	Q7YRB5	Q7yrb5 tursiops tr
39	77.5	13.2	100	13	Q8QGB7	Q8qgb7 oncorhynchu
40	77.5	13.2	125	11	Q8K4B1	Q8k4b1 rattus norv
41	77	13.1	111	13	Q8AXZ1	Q8axz1 ictalurus p
42	76.5	13.0	59	6	O62764	O62764 equus cabal
43	76	12.9	98	11	Q9ERB1	Q9erb1 mesocricetu
44	76	12.9	98	13	Q7T1P1	Q7t1p1 cyprinus ca
45	76	12.9	677	5	O18209	O18209 caenorhabdi

ALIGNMENTS

RESULT 1
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ID Q9NS21 PRELIMINARY; PRT; 111 AA.
AC Q9NS21;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Chemokine MIP-2 gamma.
GN MIP-2 GAMMA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20405642; PubMed=10946286;
RA Cao X., Zhang W., Wan T., He L., Chen T., Yuan Z., Ma S., Yu Y.,
RA Chen G.;
RT "Molecular cloning and characterization of a novel CXC chemokine
RT macrophage inflammatory protein-2gamma chemoattractant for human
RT neutrophils and dendritic cells.";
RL J. Immunol. 165:2588-2595(2000).
DR EMBL; AF106911; AAF78449.1; -.
DR PIR; JG0182; JG0182.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
SQ SEQUENCE 111 AA; 13126 MW; C9A18B3178CACF74 CRC64;

Query Match 99.1%; Score 582; DB 4; Length 111;
Best Local Similarity 99.1%; Pred. No. 1e-58;
Matches 110; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 MSLLPRRAPPVSMRLLAAALLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSLLPRRAPPVSMRLLAAALLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60
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Qy          61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
               ||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db          61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRFYEE 111


RESULT 2
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ID   Q8K453      PRELIMINARY;      PRT;    99 AA.
AC   Q8K453;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   BRAK.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Wistar;
RA   Han G.D., Koike H., Shimizu F., Kawachi H.;
RT   "Rat homolog of breast and kidney.";
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF488348; AAM74057.1; -.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0008009; F:chemokine activity; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   Pfam; PF00048; IL8; 1.
SQ   SEQUENCE   99 AA;  11730 MW;  972C06336C7F46D6 CRC64;

  Query Match             86.4%;  Score 507;  DB 11;  Length 99;
  Best Local Similarity   96.0%;  Pred. No. 3.4e-50;
  Matches   95;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          13 MRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIITT 72
               |||||||||||||||  :||||||||||||||||||||||||||||||||||||||||||
Db           1 MRLLAAALLLLLLALCASRVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIITT 60

Qy          73 KSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
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Db          61 KSMSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 99


RESULT 3
Q9JHH7
ID   Q9JHH7      PRELIMINARY;      PRT;    99 AA.
AC   Q9JHH7;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   B cell and mononcyte-activating chemokine precursor (Brain cDNA, clone
DE   MNCb-6413, similar to Mus musculus kidney-expressed chemokine CXC
DE   (Kec) mRNA) (Kec) (1200006I23Rik protein) (Small inducible cytokine
DE   subfamily B).
GN   CXCL14 OR SCYB14 OR BMAC OR 1200006I23RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/CBYJ;
RA   Sleeman M.A., Fraser J.K., Murison J.G., Kelly S.L., Prestidge R.,
RA   Watson J.D., Kumble K.D.;
RT   "B cell and monocyte-activating chemokine (BMAC), a novel non-ELR
RT   alpha chemokine.";
RL   Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL;
RA   Osada N., Kusuda J., Tanuma R., Ito A., Hirata M., Sugano S.,
RA   Hashimoto K.;
RT   "isolation of full-length cDNA clones from mouse brain cDNA library
RT   made by oligo-capping method.";
RL   Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Embryo, and Lung;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Body;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AF144754; AAF66694.1; -.
DR   EMBL; AB041614; BAA95097.1; -.
DR   EMBL; AK014351; BAB29292.1; -.
DR   EMBL; AK004615; BAB23411.1; -.
DR   EMBL; AK076112; BAC36192.1; -.
DR   MGD; MGI:1888514; Cxcl14.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0008009; F:chemokine activity; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   Pfam; PF00048; IL8; 1.
KW   Signal.
FT   SIGNAL        1     23       POTENTIAL.
FT   CHAIN        24     99       B CELL AND MONONCYTE-ACTIVATING
FT                                CHEMOKINE.
SQ   SEQUENCE   99 AA;  11716 MW;  97352E91FF7F46D6 CRC64;

  Query Match             86.2%;  Score 506;  DB 11;  Length 99;
  Best Local Similarity   94.9%;  Pred. No. 4.4e-50;
  Matches   94;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          13 MRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIITT 72
               |||||||||||||||  :||||||||||||||||||||||||||||||||||||||:||
Db           1 MRLLAAALLLLLLALCASRVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIVTT 60

Qy          73 KSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
               ||:|||||||||||||||||||||||||||||||||||
Db          61 KSMSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 99


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Q91V02
ID   Q91V02      PRELIMINARY;      PRT;    95 AA.
AC   Q91V02;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Db        246 TATCATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCTGCACCCCAA 305

Qy        430 GCTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAAGCGCAGGGT 489
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        306 GCTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAAGCGCAGGTT 365

Qy        490 CTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTGGGAGACTTG 549
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Qy        550 TG--CAAAGGACTTTGCAGATTAAAAAAAAAAAAAA 583
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Db        426 TGGCAAAGGAACTTTGCAGATTAAAAAAAAAAAAAA 461


RESULT 11
US-09-238-184-1
; Sequence 1, Application US/09238184
; Patent No. 6479633
;  GENERAL INFORMATION:
;    APPLICANT:  Ni, Jian
;    APPLICANT:  Gentz, Reiner L.
;    APPLICANT:  Su, Jeffrey Y.
;    APPLICANT:  Li, Haodong
;    TITLE OF INVENTION:  Chemokine Alpha 2
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox, P.L.L.C.
;      STREET:  1100 New York Ave., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-2934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/238,184
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/825,556
;      FILING DATE:  19-MAR-1997
;      APPLICATION NUMBER:  US 60/013,653
;      FILING DATE:  19-MAR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steffe, Eric K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.0850001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  461 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  both
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
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;      NAME/KEY:  mat_peptide
;      LOCATION:  127..375
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;      NAME/KEY:  sig_peptide
;      LOCATION:  79..126
US-09-238-184-1

  Query Match             25.9%;  Score 435.6;  DB 4;  Length 461;
  Best Local Similarity   98.7%;  Pred. No. 4.9e-93;
  Matches  450;  Conservative    0;  Mismatches    4;  Indels    2;  Gaps    1;

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Db        186 CAGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGAGAAGATGGT 245

Qy        370 TATCATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCTGCACCCCAA 429
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 TATCATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCTGCACCCCAA 305

Qy        430 GCTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAAGCGCAGGGT 489
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        306 GCTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAAGCGCAGGTT 365

Qy        490 CTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTGGGAGACTTG 549
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Db        366 CTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTGGGAGACTTG 425

Qy        550 TG--CAAAGGACTTTGCAGATTAAAAAAAAAAAAAA 583
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Db        426 TGGCAAAGGAACTTTGCAGATTAAAAAAAAAAAAAA 461


RESULT 12
US-09-188-930-38
; Sequence 38, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
;  APPLICANT: Watson, James D.
;  APPLICANT: Strachan, Lorna
;  APPLICANT: Sleeman, Matthew
;  APPLICANT: Onrust, Rene
;  APPLICANT: Murison, James Greg
;  TITLE OF INVENTION: Compositions Isolated From Skin Cells
;  TITLE OF INVENTION: and Methods For Their Use
;  FILE REFERENCE: 11000.1011c1
;  CURRENT APPLICATION NUMBER: US/09/188,930A
;  CURRENT FILING DATE: 1998-11-09
;  NUMBER OF SEQ ID NOS: 348
;  SOFTWARE: PastSEQ for Windows Version 3.0
; SEQ ID NO 38
;   LENGTH: 766
;   TYPE: DNA
;   ORGANISM: mouse
US-09-188-930-38

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  Best Local Similarity   79.5%;  Pred. No. 1.1e-90;
  Matches  606;  Conservative    0;  Mismatches  115;  Indels   41;  Gaps    7;

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GenCore version 5.1.6

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(without alignments)
260.476 Million cell updates/sec

Title: US-09-978-189-370
Perfect score: 587
Sequence: 1 MSLLPRRAPPVSMRLLAAAL.....TKRFIKWYNAWNEKRRVYEE 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	582	99.1	111	2	US-08-825-556A-2	Sequence 2, Appli
2	582	99.1	111	4	US-09-238-184-2	Sequence 2, Appli
3	522	88.9	99	2	US-08-825-556A-3	Sequence 3, Appli
4	522	88.9	99	4	US-09-238-184-3	Sequence 3, Appli
5	509	86.7	95	3	US-09-188-930-344	Sequence 344, App
6	509	86.7	95	4	US-09-724-864-68	Sequence 68, Appl
7	509	86.7	95	4	US-09-312-283C-344	Sequence 344, App
8	506	86.2	99	3	US-09-188-930-340	Sequence 340, App
9	506	86.2	99	4	US-09-312-283C-340	Sequence 340, App
10	506	86.2	99	4	US-09-312-283C-394	Sequence 394, App
11	506	86.2	99	4	US-09-312-283C-417	Sequence 417, App
12	504.5	85.9	98	4	US-09-312-283C-418	Sequence 418, App
13	428	72.9	77	3	US-09-188-930-346	Sequence 346, App
14	428	72.9	77	4	US-09-724-864-72	Sequence 72, Appl
15	428	72.9	77	4	US-09-312-283C-346	Sequence 346, App
16	424	72.2	77	3	US-09-188-930-345	Sequence 345, App
17	424	72.2	77	4	US-09-724-864-70	Sequence 70, Appl
18	424	72.2	77	4	US-09-312-283C-345	Sequence 345, App
19	414	70.5	75	4	US-09-177-304-3	Sequence 3, Appli
20	298	50.8	133	3	US-09-188-930-157	Sequence 157, App
21	298	50.8	133	4	US-09-312-283C-157	Sequence 157, App
22	143.5	24.4	98	2	US-08-825-556A-4	Sequence 4, Appli
23	143.5	24.4	98	4	US-09-238-184-4	Sequence 4, Appli
24	143.5	24.4	100	4	US-08-679-493A-146	Sequence 146, App
25	138	23.5	100	3	US-08-476-376-2	Sequence 2, Appli
26	138	23.5	100	4	US-09-312-283C-423	Sequence 423, App
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29	128.5	21.9	107	2	US-08-468-819-6	Sequence 6, Appli
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36	117.5	20.0	107	3	US-09-203-235-7	Sequence 7, Appli
37	117.5	20.0	107	4	US-09-213-383-5	Sequence 5, Appli
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39	113	19.3	71	2	US-08-812-003-9	Sequence 9, Appli
40	111	18.9	96	4	US-08-649-006A-7	Sequence 7, Appli
41	111	18.9	96	4	US-09-771-023-9	Sequence 9, Appli
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ALIGNMENTS

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RESULT 1
US-08-825-556A-2
; Sequence 2, Application US/08825556A
; Patent No. 5910431
;  GENERAL INFORMATION:
;    APPLICANT:  Ni, Jian
;    APPLICANT:  Gentz, Reiner L.
;    APPLICANT:  Su, Jeffrey Y.
;    APPLICANT:  Li, Haodong
;    TITLE OF INVENTION:  Chemokine Alpha 2
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox, P.L.L.C.
;      STREET:  1100 New York Ave., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-2934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/825,556A
;      FILING DATE:  19-MAR-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/013,653
;      FILING DATE:  19-MAR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steffe, Eric K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.0850001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  111 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-825-556A-2

  Query Match           99.1%;  Score 582;  DB 2;  Length 111;
  Best Local Similarity  99.1%;  Pred. No. 1.4e-63;
  Matches 110;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60
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Qy         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
                ||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRFYEE 111


RESULT 2
US-09-238-184-2
; Sequence 2, Application US/09238184
; Patent No. 6479633
;  GENERAL INFORMATION:
;    APPLICANT:  Ni, Jian
;    APPLICANT:  Gentz, Reiner L.
;    APPLICANT:  Su, Jeffrey Y.
;    APPLICANT:  Li, Haodong
;    TITLE OF INVENTION:  Chemokine Alpha 2
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox, P.L.L.C.
;      STREET:  1100 New York Ave., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-2934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/238,184
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/825,556
;      FILING DATE:  19-MAR-1997
;      APPLICATION NUMBER:  US 60/013,653
;      FILING DATE:  19-MAR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steffe, Eric K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.0850001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  111 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-238-184-2

  Query Match             99.1%;  Score 582;  DB 4;  Length 111;
  Best Local Similarity   99.1%;  Pred. No. 1.4e-63;
  Matches  110;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60

Qy         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
                ||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRFYEE 111


RESULT 3
US-08-825-556A-3
; Sequence 3, Application US/08825556A
; Patent No. 5910431
;  GENERAL INFORMATION:
;    APPLICANT:  Ni, Jian
;    APPLICANT:  Gentz, Reiner L.
;    APPLICANT:  Su, Jeffrey Y.
;    APPLICANT:  Li, Haodong
;    TITLE OF INVENTION:  Chemokine Alpha 2
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox, P.L.L.C.
;      STREET:  1100 New York Ave., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-2934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/825,556A
;      FILING DATE:  19-MAR-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/013,653
;      FILING DATE:  19-MAR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steffe, Eric K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.0850001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  99 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-825-556A-3

  Query Match             88.9%;  Score 522;  DB 2;  Length 99;
  Best Local Similarity   99.0%;  Pred. No. 2.6e-56;
  Matches   98;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         13 MRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIITT 72
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Db          1 MRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIITT 60

Qy         73 KSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
              ||||||||||||||||||||||||||||||||||| |||
Db         61 KSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRFYEE 99


RESULT 4
US-09-238-184-3
; Sequence 3, Application US/09238184
; Patent No. 6479633
;  GENERAL INFORMATION:
;    APPLICANT:  Ni, Jian
;    APPLICANT:  Gentz, Reiner L.
;    APPLICANT:  Su, Jeffrey Y.
;    APPLICANT:  Li, Haodong
;    TITLE OF INVENTION:  Chemokine Alpha 2
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox, P.L.L.C.
;      STREET:  1100 New York Ave., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-2934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 22, 2004, 12:29:47 ; Search time 40 Seconds
(without alignments)
875.563 Million cell updates/sec

Title: US-09-978-189-370
Perfect score: 587
Sequence: 1 MSLLPRRAPPVSMRLLAAAL.....TKRFIKWYNAWNEKRRVYEE 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	582	99.1	111	4	Q9NS21	Q9ns21 homo sapien
2	507	86.4	99	11	Q8K453	Q8k453 rattus norv
3	506	86.2	99	11	Q9JHH7	Q9jhh7 mus musculu
4	488	83.1	95	11	Q91V02	Q91v02 mus musculu
5	335	57.1	100	13	Q9DFG4	Q9dfg4 brachydanio
6	322.5	54.9	98	13	Q9DGL8	Q9dgl8 gallus gall
7	143.5	24.4	101	11	Q9EP62	Q9ep62 rattus norv
8	128.5	21.9	108	6	Q28724	Q28724 oryctolagus
9	128	21.8	100	11	Q91ZK9	Q91zk9 sigmodon hi
10	126.5	21.6	101	11	Q91Z64	Q91z64 sigmodon hi
11	121.5	20.7	107	6	Q8HXZ4	Q8hxz4 macaca mula
12	119.5	20.4	107	6	Q8HXZ3	Q8hxz3 macaca mula
13	100	17.0	95	13	Q7T0B3	Q7t0b3 ictalurus p
14	97.5	16.6	97	13	Q98TQ2	Q98tq2 oncorhynchu
15	94.5	16.1	97	13	Q7SX73	Q7sx73 oncorhynchu
16	94.5	16.1	113	6	Q8MIN2	Q8min2 equus cabal
17	93.5	15.9	126	11	Q99J60	Q99j60 mus musculu
18	89.5	15.2	97	13	Q8QFP5	Q8qfp5 cyprinus ca
19	89.5	15.2	100	13	Q8AXP4	Q8axp4 chimaera ph
20	89.5	15.2	126	11	Q8C9J0	Q8c9j0 mus musculu
21	89	15.2	95	13	Q7T0B4	Q7t0b4 ictalurus p
22	89	15.2	113	11	Q9EQI5	Q9eqi5 mus musculu
23	88	15.0	95	13	Q7T0B2	Q7t0b2 ictalurus f
24	88	15.0	109	13	Q90Y59	Q90y59 paralichthy
25	87.5	14.9	111	11	Q99ME0	Q99me0 rattus norv
26	87	14.8	98	13	Q8QGV8	Q8qgv8 paralichthy
27	86.5	14.7	104	13	O73912	O73912 gallus gall
28	86	14.7	93	13	Q9PTF8	Q9ptf8 brachydanio
29	84.5	14.4	116	11	Q91ZB2	Q91zb2 mus musculu
30	84.5	14.4	117	11	Q8C9B8	Q8c9b8 mus musculu
31	83.5	14.2	102	6	Q95MZ7	Q95mz7 ovis aries
32	83.5	14.2	102	6	Q867B3	Q867b3 capra hircu
33	83.5	14.2	117	12	Q68398	Q68398 human cytom
34	83	14.1	94	6	Q8MIZ0	Q8miz0 macaca mula
35	81.5	13.9	101	13	Q8UW91	Q8uw91 triakis scy
36	80.5	13.7	98	6	Q8MIZ1	Q8miz1 macaca mula
37	80.5	13.7	98	6	Q865F5	Q865f5 macaca neme
38	79.5	13.5	101	6	Q7YRB5	Q7yrb5 tursiops tr
39	77.5	13.2	100	13	Q8QGB7	Q8qgb7 oncorhynchu
40	77.5	13.2	125	11	Q8K4B1	Q8k4b1 rattus norv
41	77	13.1	111	13	Q8AXZ1	Q8axz1 ictalurus p
42	76.5	13.0	59	6	O62764	O62764 equus cabal
43	76	12.9	98	11	Q9ERB1	Q9erb1 mesocricetu
44	76	12.9	98	13	Q7T1P1	Q7t1p1 cyprinus ca
45	76	12.9	677	5	O18209	O18209 caenorhabdi

ALIGNMENTS

RESULT 1
Q9NS21
ID Q9NS21 PRELIMINARY; PRT; 111 AA.
AC Q9NS21;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Chemokine MIP-2 gamma.
GN MIP-2 GAMMA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20405642; PubMed=10946286;
RA Cao X., Zhang W., Wan T., He L., Chen T., Yuan Z., Ma S., Yu Y.,
RA Chen G.;
RT "Molecular cloning and characterization of a novel CXC chemokine
RT macrophage inflammatory protein-2gamma chemoattractant for human
RT neutrophils and dendritic cells.";
RL J. Immunol. 165:2588-2595(2000).
DR EMBL; AF106911; AAF78449.1; -.
DR PIR; JG0182; JG0182.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
SQ SEQUENCE 111 AA; 13126 MW; C9A18B3178CACF74 CRC64;

Query Match 99.1%; Score 582; DB 4; Length 111;
Best Local Similarity 99.1%; Pred. No. 1e-58;
Matches 110; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60
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```
Qy          61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
               ||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db          61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRFYEE 111
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RESULT 2
Q8K453
ID Q8K453 PRELIMINARY; PRT; 99 AA.
AC Q8K453;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE BRAK.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar;
RA Han G.D., Koike H., Shimizu F., Kawachi H.;
RT "Rat homolog of breast and kidney.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF488348; AAM74057.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
SQ SEQUENCE 99 AA; 11730 MW; 972C06336C7F46D6 CRC64;

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  Query Match             86.4%;  Score 507;  DB 11;  Length 99;
  Best Local Similarity   96.0%;  Pred. No. 3.4e-50;
  Matches   95;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          13 MRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIITT 72
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Db           1 MRLLAAALLLLLLALCASRVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIITT 60

Qy          73 KSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
               ||:|||||||||||||||||||||||||||||||||||
Db          61 KSMSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 99
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RESULT 3
Q9JHH7
ID Q9JHH7 PRELIMINARY; PRT; 99 AA.
AC Q9JHH7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE B cell and mononcyte-activating chemokine precursor (Brain cDNA, clone
DE MNCb-6413, similar to Mus musculus kidney-expressed chemokine CXC
DE (Kec) mRNA) (Kec) (1200006I23Rik protein) (Small inducible cytokine
DE subfamily B).
GN CXCL14 OR SCYB14 OR BMAC OR 1200006I23RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CBYJ;
RA Sleeman M.A., Fraser J.K., Murison J.G., Kelly S.L., Prestidge R.,
RA Watson J.D., Kumble K.D.;
RT "B cell and monocyte-activating chemokine (BMAC), a novel non-ELR
RT alpha chemokine.";
RL Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL;
RA Osada N., Kusuda J., Tanuma R., Ito A., Hirata M., Sugano S.,
RA Hashimoto K.;
RT "isolation of full-length cDNA clones from mouse brain cDNA library
RT made by oligo-capping method.";
RL Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo, and Lung;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Body;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AF144754; AAF66694.1; -.
DR EMBL; AB041614; BAA95097.1; -.
DR EMBL; AK014351; BAB29292.1; -.
DR EMBL; AK004615; BAB23411.1; -.
DR EMBL; AK076112; BAC36192.1; -.
DR MGD; MGI:1888514; Cxcl14.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 99 B CELL AND MONONCYTE-ACTIVATING
FT CHEMOKINE.
SQ SEQUENCE 99 AA; 11716 MW; 97352E91FF7F46D6 CRC64;

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  Query Match             86.2%;  Score 506;  DB 11;  Length 99;
  Best Local Similarity   94.9%;  Pred. No. 4.4e-50;
  Matches   94;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          13 MRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIITT 72
               |||||||||||||||  :|||||||||||||||||||||||||||||||||||||||:||
Db           1 MRLLAAALLLLLLALCASRVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIVTT 60

Qy          73 KSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
               ||:|||||||||||||||||||||||||||||||||||
Db          61 KSMSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 99
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RESULT 4
Q91V02
ID Q91V02 PRELIMINARY; PRT; 95 AA.
AC Q91V02;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 26, 2004, 03:16:23 ; Search time 694 Seconds
(without alignments)
10314.429 Million cell updates/sec

Title: US-09-978-189-369
Perfect score: 1685
Sequence: 1 gcggagacaagcgcagagcg.....aatgtaaaaaaaaaaaaaaa 1685

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1685	100.0	1685	2	AAZ34205	Aaz34205 Human PRO
2	1685	100.0	1685	3	AAC58588	Aac58588 Human PRO
3	1685	100.0	1685	3	AAC78551	Aac78551 Human PRO
4	1685	100.0	1685	6	ABS55212	Abs55212 Human Bol
5	1685	100.0	1685	7	ACD42738	Acd42738 Novel hum
6	1685	100.0	1685	7	ACA63773	Aca63773 Novel hum
7	1685	100.0	1685	7	ABV72423	Abv72423 Nucleotid
8	1685	100.0	1685	7	ACA71937	Aca71937 Human sec
9	1685	100.0	1685	7	ABX92577	Abx92577 cDNA enco
10	1685	100.0	1685	7	ACA66318	Aca66318 Human cDN
11	1685	100.0	1685	8	ADA24908	Ada24908 Novel hum
12	1685	100.0	1685	8	ACD29919	Acd29919 Novel hum
13	1685	100.0	1685	8	ADA12569	Ada12569 Human cDN
14	1685	100.0	1685	8	ACD29334	Acd29334 Novel hum
15	1685	100.0	1685	9	ADB73875	Adb73875 Human PRO
16	1685	100.0	1685	9	ADB76591	Adb76591 Human PRO
17	1685	100.0	1685	9	ADC44017	Adc44017 Human cDN
18	1685	100.0	1685	9	ADC61777	Adc61777 Human cDN
19	1685	100.0	1685	9	ADC63741	Adc63741 Human cDN
20	1685	100.0	1685	9	ADC66841	Adc66841 Human cDN
21	1685	100.0	1685	9	ADC68965	Adc68965 Human cDN
22	1685	100.0	1685	9	ADC63025	Adc63025 Human cDN
23	1685	100.0	1685	9	ADC68090	Adc68090 Human cDN
24	1685	100.0	1685	9	ADC41410	Adc41410 Human cDN
25	1685	100.0	1685	9	ADC67465	Adc67465 Human cDN
26	1685	100.0	1685	9	ADC62401	Adc62401 Human cDN
27	1685	100.0	1685	9	ADC42034	Adc42034 Human cDN
28	1685	100.0	1685	9	ADE49403	Ade49403 Human cDN
29	1685	100.0	1685	9	ADE35457	Ade35457 Human cDN
30	1685	100.0	1685	9	ADE16571	Ade16571 Human cDN
31	1685	100.0	1685	9	ADD73186	Add73186 Human cDN
32	1685	100.0	1685	9	ADD72544	Add72544 Human cDN
33	1685	100.0	1685	9	ADE17195	Ade17195 Human cDN
34	1685	100.0	1685	10	ADE48703	Ade48703 Human cDN
35	1685	100.0	1685	10	ADE89804	Ade89804 Human cDN
36	1640.4	97.4	1677	5	AAF93905	Aaf93905 Human cDN
37	1447	85.9	1564	2	AAZ08962	Aaz08962 Human neo
38	1447	85.9	1564	7	ABX10886	Abx10886 cDNA enco
39	1358.4	80.6	1458	2	AAZ08965	Aaz08965 Macaque n
40	1358.4	80.6	1458	7	ABX10892	Abx10892 cDNA enco
41	1178.8	70.0	14962	6	ABN88003	Abn88003 Human sma
42	1092.2	64.8	1630	2	AAZ42039	Aaz42039 Human end
43	974.6	57.8	1962	2	AAZ52934	Aaz52934 Human pro
c 44	872.6	51.8	1962	2	AAZ52934	Aaz52934 Human pro
45	727.2	43.2	1663	3	AAZ61823	Aaz61823 Full-leng

ALIGNMENTS

RESULT 1
AAZ34205
ID AAZ34205 standard; cDNA; 1685 BP.
XX
AC AAZ34205;
XX
DT 07-DEC-1999 (first entry)
XX
DE Human PRO273 nucleotide sequence.
XX
KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW secreted protein; transmembrane protein; ss.
XX
OS Homo sapiens.
XX
PN WO9946281-A2.
XX
PD 16-SEP-1999.
XX
PF 08-MAR-1999; 99WO-US005028.
XX
PR 10-MAR-1998; 98US-0077450P.
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PR 17-MAR-1998; 98US-00040220.
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PR 29-APR-1998; 98US-0083500P.
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PR 05-MAY-1998; 98US-0084366P.
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PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085689P.
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PR 22-MAY-1998; 98US-0086392P.
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PR 22-MAY-1998; 98US-0086430P.
PR 22-MAY-1998; 98US-0086486P.
PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087106P.
PR 28-MAY-1998; 98US-0087208P.
PR 30-JUL-1998; 98US-0094651P.
PR 11-SEP-1998; 98US-0100038P.
XX
PA (GETH) GENENTECH INC.
XX
PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX
DR WPI; 1999-551358/46.
DR P-PSDB; AAY41739.
XX
PT New secreted and transmembrane polypeptides and their polynucleotides,
PT useful for treating blood coagulation disorders, cancers and cellular
PT adhesion disorders.
XX
PS Claim 2; Fig 148; 530pp; English.
XX
CC The present invention describes secreted and transmembrane polypeptides
CC and their polynucleotides. The nucleotide sequences are useful as sources
CC of probes, primers, for chromosome mapping, and for generation of
CC antisense sequences. They can also be used to create transgenic animals.
CC The proteins can be used to treat a variety of diseases and disorders,
CC depending on their function. Diseases that may be treated include blood
CC coagulation disorders, cancers and cellular adhesion disorders. They may
CC also be used to raise antibodies. AAZ33891 to AAZ34338, and AAY41685 to
CC AAY41774 represent polynucleotide and polypeptide sequence given in the
CC exemplification of the present invention
XX
SQ Sequence 1685 BP; 484 A; 435 C; 387 G; 379 T; 0 U; 0 Other;

Query Match 100.0%; Score 1685; DB 2; Length 1685;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1685; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGG 60
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Db          1 GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGG 60

Qy         61 CGCAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCT 120
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Db         61 CGCAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCT 120

Qy        121 GGGTGGCGTCTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCC 180
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Db        121 GGGTGGCGTCTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCC 180

Qy        181 ACGCCGCGCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCT 240
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Db        181 ACGCCGCGCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCT 240

Qy        241 GGCGCTGTACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAA 300
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Db        241 GGCGCTGTACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAA 300

Qy        301 GATCCGCTACAGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGA 360
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Db        301 GATCCGCTACAGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGA 360

Qy        361 GAAGATGGTTATCATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCT 420
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Db        361 GAAGATGGTTATCATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCT 420

Qy        421 GCACCCCAAGCTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAA 480
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Db        421 GCACCCCAAGCTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAA 480

Qy        481 GCGCAGGGTCTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTG 540
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Db        481 GCGCAGGGTCTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTG 540

Qy        541 GGAGACTTGTGCAAAGGACTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 600
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Db        541 GGAGACTTGTGCAAAGGACTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 600

Qy        601 AAAAAAAAAAAAAGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGA 660
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Db        601 AAAAAAAAAAAAAGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGA 660

Qy        661 AGCACTTTTTACCAACGGTCAGTTTTTACATTTATAGCTGCGTGCGAAAGGCTTCCAGA 720
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Db        661 AGCACTTTTTACCAACGGTCAGTTTTTACATTTATAGCTGCGTGCGAAAGGCTTCCAGA 720

Qy        721 TGGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGG 780
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Db        721 TGGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGG 780
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Qy        781 GGAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTA 840
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Db        781 GGAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTA 840

Qy        841 TACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTG 900
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Db        841 TACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTG 900

Qy        901 CAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCAC 960
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Qy        961 AGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTG 1020
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Qy       1021 GCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAA 1080
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Qy       1081 GTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGA 1140
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Qy       1141 AACATTTCCAAGATCCTGTGATGGCGAGACAAATGATCCTTAAAGAAGGTGTGGGGTCTT 1200
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Qy       1201 TCCCAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATATTTAATGCTTCAGAAGCATG 1260
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Qy       1261 TGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATATGAATACA 1320
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Db       1261 TGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATATGAATACA 1320

Qy       1321 TGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGT 1380
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Db       1321 TGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGT 1380

Qy       1381 TTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATATTTGTGATTCCCCAT 1440
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Db       1381 TTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATATTTGTGATTCCCCAT 1440

Qy       1441 GTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGATGACCATGCGCCC 1500
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Qy       1501 TTTCCTCTGTACATATACCCTTAAGAACGCCCCCTCCACACACTGCCCCCCAGTATATGC 1560
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Qy       1621 GGTTTCATATTCTTTCTAAGATGGAAAGTAATAAAATATATTTGAAATGTAAAAAAAAAA 1680
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Db       1621 GGTTTCATATTCTTTCTAAGATGGAAAGTAATAAAATATATTTGAAATGTAAAAAAAAAA 1680

Qy       1681 AAAAA 1685
              |||||
Db       1681 AAAAA 1685
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RESULT 2
AAC58588
ID AAC58588 standard; cDNA; 1685 BP.
XX
AC AAC58588;
XX
DT 29-JAN-2001 (first entry)

XX
DE Human PRO273 protein UNQ240 encoding cDNA SEQ ID NO:45.
XX
KW Human; immune related disease; diagnosis; antiinflammatory; cardiant;
KW dermatological; antiarthritic; antirheumatic; immunosuppressive;
KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
KW antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;
KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
KW osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
KW autoimmune thrombocytopaenia; immune-mediated renal disease;
KW demyelinating disease; hepatobiliary disease; Whipple's disease;
KW inflammatory bowel disease; gluten-sensitive enteropathy;
KW autoimmune disease; immune-mediated skin disease; allergic disease;
KW immunological disease; transplantation associated disease;
KW graft rejection; graft-versus-host-disease; ss.
XX
OS Homo sapiens.
XX
PN WO200053758-A2.
XX
PD 14-SEP-2000.
XX
PF 02-MAR-2000; 2000WO-US005841.
XX
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99US-0123618P.
PR 12-MAR-1999; 99US-0123957P.
PR 23-MAR-1999; 99US-0125775P.
PR 12-APR-1999; 99US-0128849P.
PR 20-APR-1999; 99WO-US008615.
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PR 08-SEP-1999; 99WO-US020594.
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PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-OCT-1999; 99US-0162506P.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
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PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;
XX
DR WPI; 2000-572271/53.

DR P-PSDB; AAB33423.
XX
PT Sixty four PRO polypeptides, useful in the diagnosis and treatment of
PT immune related disorders, e.g. systemic lupus erythematosis, rheumatoid
PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
XX
PS Claim 23; Fig 19; 309pp; English.
XX
CC The present invention describes sixty four human PRO proteins which can
CC be used in the treatment of immune related diseases. The human PRO
CC proteins, anti-PRO antibodies, agonists and antagonists are useful for
CC treating and diagnosing immune related disorders. The disorders are
CC selected from systemic lupus erythematosus, rheumatoid arthritis,
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
CC anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
CC immune-mediated renal disease, demyelinating diseases of the central and
CC peripheral nervous systems, hepatobiliary diseases, inflammatory bowel
CC disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune
CC or immune-mediated skin diseases, allergic diseases, immunological
CC diseases of the lung, and transplantation associated diseases including
CC graft rejection and graft-versus-host-disease. AAC58397 to AAC58578
CC represent PCR primers and hybridisation probes used in the isolation of
CC human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477
CC represent human PRO polynucleotide and protein sequences given in the
CC exemplification of the present invention
XX
SQ Sequence 1685 BP; 484 A; 435 C; 387 G; 379 T; 0 U; 0 Other;

Query Match 100.0%; Score 1685; DB 3; Length 1685;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1685; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGG 60
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Db          1 GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGG 60

Qy         61 CGCAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCT 120
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Db         61 CGCAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCT 120

Qy        121 GGGTGGCGTCTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCC 180
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Db        121 GGGTGGCGTCTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCC 180

Qy        181 ACGCCGCGCCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCT 240
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Db        181 ACGCCGCGCCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCT 240

Qy        241 GGCGCTGTACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAA 300
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Db        241 GGCGCTGTACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAA 300

Qy        301 GATCCGCTACAGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GATCCGCTACAGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGA 360

Qy        361 GAAGATGGTTATCATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCT 420
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Qy        421 GCACCCCAAGCTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAA 480
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Db        421 GCACCCCAAGCTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAA 480

Qy        481 GCGCAGGGTCTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTG 540
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Db        481 GCGCAGGGTCTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTG 540

Qy        541 GGAGACTTGTGCAAAGGACTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGAGACTTGTGCAAAGGACTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 600

Qy        601 AAAAAAAAAAAAAGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAAAAAAAAAAAAGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGA 660

Qy        661 AGCACTTTTTACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGCACTTTTTACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGA 720

Qy        721 TGGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTTATCAAAAAGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTTATCAAAAAGG 780

Qy        781 GGAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GGAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTA 840

Qy        841 TACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTG 900

Qy        901 CAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCAC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCAC 960

Qy        961 AGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTG 1020

Qy       1021 GCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAA 1080

Qy       1081 GTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGA 1140

Qy       1141 AACATTTCCAAGATCCTGTGATGGCGAGACAAATGATCCTTAAAGAAGGTGTGGGGTCTT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AACATTTCCAAGATCCTGTGATGGCGAGACAAATGATCCTTAAAGAAGGTGTGGGGTCTT 1200

Qy       1201 TCCCAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATATTTAATGCTTCAGAAGCATG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TCCCAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATATTTAATGCTTCAGAAGCATG 1260

Qy       1261 TGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATATGAATACA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATATGAATACA 1320

Qy       1321 TGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGT 1380

Qy       1381 TTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATATTTGTGATTCCCCAT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATATTTGTGATTCCCCAT 1440

Qy       1441 GTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGATGACCATGCGCCC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGATGACCATGCGCCC 1500

Qy       1501 TTTCCTCTGTACATATACCCTTAAGAACGCCCCCTCCACACACTGCCCCCCAGTATATGC 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 TTTCCTCTGTACATATACCCTTAAGAACGCCCCCTCCACACACTGCCCCCCAGTATATGC 1560

Qy       1561 CGCATTGTACTGCTGTGTTTATATGCTATGTACATGTCAGAAACCATTAGCATTGCATGCA 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CGCATTGTACTGCTGTGTTTATATGCTATGTACATGTCAGAAACCATTAGCATTGCATGCA 1620

Qy       1621 GGTTTCATATTCTTTCTAAGATGGAAAGTAATAAAATATATTTGAAATGTAAAAAAAAAA 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GGTTTCATATTCTTTCTAAGATGGAAAGTAATAAAATATATTTGAAATGTAAAAAAAAAA 1680
```

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Qy       1681 AAAAA 1685
              |||||
Db       1681 AAAAA 1685
```

RESULT 3
AAC78551
ID AAC78551 standard; cDNA; 1685 BP.
XX
AC AAC78551;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human PRO273 (UNQ240) nucleotide sequence SEQ ID NO:369.
XX
KW Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;
KW expressed sequence tag; detection; cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200053756-A2.
XX
PD 14-SEP-2000.
XX
PF 18-FEB-2000; 2000WO-US004341.
XX
PR 08-MAR-1999; 99WO-US005028.
PR 12-MAR-1999; 99US-0123957P.
PR 29-MAR-1999; 99US-0126773P.
PR 21-APR-1999; 99US-0130232P.
PR 28-APR-1999; 99US-0131445P.
PR 14-MAY-1999; 99US-0134287P.
PR 23-JUN-1999; 99US-0141037P.
PR 26-JUL-1999; 99US-0145698P.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR WPI; 2000-611443/58.
DR P-PSDB; AAB44295.
XX
PT Novel PRO polypeptides and polynucleotides used in detection methods, to
PT target bioactive molecules to specific cells, and to modulate cellular
PT activities.
XX
PS Claim 2; Fig 148; 636pp; English.
XX
CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence
CC tag) sequences which encode secreted or transmembrane PRO polypeptides.
CC The PRO polynucleotides and polypeptides have cytostatic activity. The
CC polynucleotides and polypeptides can be used for detecting the presence
CC of PRO polypeptides in samples, for linking bioactive molecules to cells
CC and for modulating biological activities of cells, using the polypeptides
CC for specific targeting. The polypeptide targeting can be used to kill the
CC target cells, e.g. for the treatment of cancers. The polypeptide pairs
CC provide specific targeting of bioactive molecules to cells. AAC78600 to
CC AAC78987 represent PCR primers and probes used in the isolation of the
CC PRO polynucleotide sequences
XX
SQ Sequence 1685 BP; 484 A; 435 C; 387 G; 379 T; 0 U; 0 Other;

Query Match 100.0%; Score 1685; DB 3; Length 1685;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1685; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGG 60

Qy         61 CGCAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGCAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCT 120

Qy        121 GGGTGGCGTCTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGTGGCGTCTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCC 180

Qy        181 ACGCCGCGCCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACGCCGCGCCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCT 240

Qy        241 GGCGCTGTACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGCGCTGTACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAA 300

Qy        301 GATCCGCTACAGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GATCCGCTACAGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGA 360

Qy        361 GAAGATGGTTATCATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAAGATGGTTATCATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCT 420

Qy        421 GCACCCCAAGCTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCACCCCAAGCTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAA 480

Qy        481 GCGCAGGGTCTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCGCAGGGTCTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTG 540

Qy        541 GGAGACTTGTGCAAAGGACTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGAGACTTGTGCAAAGGACTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 600

Qy        601 AAAAAAAAAAAAAGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAAAAAAAAAAAAGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGA 660

Qy        661 AGCACTTTTTACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGCACTTTTTACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGA 720

Qy        721 TGGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGG 780

Qy        781 GGAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GGAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTA 840

Qy        841 TACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTG 900

Qy        901 CAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCAC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCAC 960

Qy        961 AGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        961 AGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTG 1020

Qy       1021 GCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAA 1080

Qy       1081 GTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGA 1140

Qy       1141 AACATTTCCAAGATCCTGTGATGGCGAGACAAATGATCCTTAAAGAAGGTGTGGGGTCTT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AACATTTCCAAGATCCTGTGATGGCGAGACAAATGATCCTTAAAGAAGGTGTGGGGTCTT 1200

Qy       1201 TCCCAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATATTTAATGCTTCAGAAGCATG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TCCCAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATATTTAATGCTTCAGAAGCATG 1260

Qy       1261 TGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATATGAATACA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATATGAATACA 1320

Qy       1321 TGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGT 1380

Qy       1381 TTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATATTTGTGATTCCCCAT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATATTTGTGATTCCCCAT 1440

Qy       1441 GTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGATGACCATGCGCCC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGATGACCATGCGCCC 1500

Qy       1501 TTTCCTCTGTACATATACCCTTAAGAACGCCCCCTCCACACACTGCCCCCCAGTATATGC 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 TTTCCTCTGTACATATACCCTTAAGAACGCCCCCTCCACACACTGCCCCCCAGTATATGC 1560

Qy       1561 CGCATTGTACTGCTGTGTTATATGCTATGTACATGTCAGAAACCATTAGCATTGCATGCA 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CGCATTGTACTGCTGTGTTATATGCTATGTACATGTCAGAAACCATTAGCATTGCATGCA 1620

Qy       1621 GGTTTCATATTCTTTCTAAGATGGAAAGTAATAAAATATATTTGAAATGTAAAAAAAAAA 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GGTTTCATATTCTTTCTAAGATGGAAAGTAATAAAATATATTTGAAATGTAAAAAAAAAA 1680

Qy       1681 AAAAA 1685
              |||||
Db       1681 AAAAA 1685
```

RESULT 4
ABS55212
ID ABS55212 standard; cDNA; 1685 BP.
XX
AC ABS55212;
XX
DT 16-DEC-2002 (first entry)
XX
DE Human Bolekine cDNA.
XX
KW Human; gene; ss; Bolekine; leukocyte; immune response; chemokine;
KW leukocyte trafficking; adhesion; endothelial cell; chemoattractant;
KW proliferation; activation; systemic lupus erythematosus; arthritis;
KW angiogenesis; systemic sclerosis; autoimmune haemolytic anaemia;
KW thyroiditis; diabetes mellitus; renal disease; demyelinating disease;
KW nervous system; polyneuropathy; hepatitis; primary biliary cirrhosis;
KW inflammatory bowel disease; autoimmune skin disease; alopecia; psoriasis;
KW allergy; asthma; atopic dermatitis; food hypersensitivity; lung disease;
KW stroke; encephalitis; multiple sclerosis; agonist; antagonist;
KW T-lymphocyte; mononuclear cell; eosinophil; polymorphonuclear neutrophil;
KW PMN; pluripotent cell; neuronal cell; MAP2; transgenic; therapeutic;
KW gene therapy; tumour; neovascularisation.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   167. .502
FT   /*tag= a
FT   /product= "Bolekine"
FT sig_peptide   167. .268
FT   /*tag= b
XX
PN US2002119118-A1.
XX
PD 29-AUG-2002.
XX
PF 22-MAR-2001; 2001US-00816920.
XX
PR 03-NOV-1997;   97US-0064249P.
PR 27-APR-1998;   98US-0083336P.
PR 08-MAR-1999;   99WO-US005028.
PR 18-FEB-2000; 2000WO-US004341.
PR 02-MAR-2000; 2000WO-US005841.
XX
PA (GETH) GENENTECH INC.
XX
PI Fong S, Goddard A, Hillan KJ, Roth I, Wood WI;
XX
DR WPI; 2002-740172/80.
DR P-PSDB; ABG70798.
XX
PT Novel Bolekine polypeptide useful for identifying agonist and antagonist
PT of the polypeptide, and for treating immune related disorder, e.g.
PT systemic lupus erythematosus and rheumatoid arthritis in a mammal.
XX
PS Claim 3; Fig 1; 63pp; English.
XX
CC The invention discloses a human Bolekine polypeptide, or its fragment.
CC Leukocytes play a important role in the immune response and the processes
CC by which these cells move to their appropriate destination is critical.
CC Chemokines are involved in leukocyte trafficking by mediating the
CC expression of adhesion molecules on endothelial cells, producing
CC chemoattractants, stimulate proliferation and regulate activation of
CC specific cell types. The polynucleotide, polypeptide and antibodies
CC raised against the polypeptide are useful for treating an immune related
CC disorder in a mammal, such as systemic lupus erythematosus, arthritis,
CC angiogenesis, systemic sclerosis, autoimmune haemolytic anaemia,
CC thyroiditis, diabetes mellitus, renal disease, demyelinating disease of
CC the central or peripheral nervous system, polyneuropathy, hepatitis,
CC primary biliary cirrhosis, inflammatory bowel disease, an autoimmune or
CC immune-mediated skin disease, alopecia, psoriasis, allergic disease,
CC asthma, atopic dermatitis, food hypersensitivity, immunologic disease of
CC the lung, stroke, encephalitis and multiple sclerosis. The polypeptides
CC and polynucleotides are also useful for identifying a compound (agonist
CC or antagonist) that inhibits the expression of activity of Bolekine, for
CC diagnosing an immune related disease in a mammal, for modulating the
CC proliferation of T-lymphocytes for enhancing the infiltration of
CC inflammatory cells (such as mononuclear cells, eosinophils and
CC polymorphonuclear neutrophils (PMNs)) into a tissue of a mammal and for
CC inducing the differentiation of pluripotent cells into neuronal cells in
CC a mammal, where the cells differentiate to a state such that neuronal
CC markers (e.g. MAP2) are detected. The polynucleotides are also useful for
CC generating transgenic or knock out animals which can be used in the
CC development and screening of therapeutically useful agents, in gene
CC therapy, chromosome markers and diagnostically for tissue typing and for
CC treating tumours by inhibiting the neovascularisation. The sequence
CC presented is the human Bolekine cDNA
XX
SQ Sequence 1685 BP; 484 A; 435 C; 387 G; 379 T; 0 U; 0 Other;

  Query Match   100.0%; Score 1685; DB 6; Length 1685;
  Best Local Similarity 100.0%; Pred. No. 0;
  Matches 1685; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy          1 GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGG 60
```

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Db       1 GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGG 60
Qy      61 CGCAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCT 120
Db      61 CGCAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCT 120
Qy     121 GGGTGGCGTCTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCC 180
Db     121 GGGTGGCGTCTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCC 180
Qy     181 ACGCCGCGCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCT 240
Db     181 ACGCCGCGCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCT 240
Qy     241 GGCGCTGTACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAA 300
Db     241 GGCGCTGTACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAA 300
Qy     301 GATCCGCTACAGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGA 360
Db     301 GATCCGCTACAGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGA 360
Qy     361 GAAGATGGTTATCATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCT 420
Db     361 GAAGATGGTTATCATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCT 420
Qy     421 GCACCCCAAGCTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAA 480
Db     421 GCACCCCAAGCTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAA 480
Qy     481 GCGCAGGGTCTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTG 540
Db     481 GCGCAGGGTCTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTG 540
Qy     541 GGAGACTTGTGCAAAGGACTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 600
Db     541 GGAGACTTGTGCAAAGGACTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 600
Qy     601 AAAAAAAAAAAAAGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGA 660
Db     601 AAAAAAAAAAAAAGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGA 660
Qy     661 AGCACTTTTTACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGA 720
Db     661 AGCACTTTTTACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGA 720
Qy     721 TGGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTTATCAAAAAGG 780
Db     721 TGGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTTATCAAAAAGG 780
Qy     781 GGAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTA 840
Db     781 GGAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTA 840
Qy     841 TACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTG 900
Db     841 TACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTG 900
Qy     901 CAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCAC 960
Db     901 CAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCAC 960
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Qy    1081 GTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGA 1140
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Db    1681 AAAAA 1685
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RESULT 5
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ID ACD42738 standard; cDNA; 1685 BP.
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AC ACD42738;
XX
DT 09-SEP-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO273 cDNA.
XX
KW Human; secreted and transmembrane protein; PRO; virucide; gene therapy;
KW cell death; growth induction cascade; blood coagulation cascade;
KW viral infection; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003050239-A1.
XX
PD 13-MAR-2003.
XX
PF 15-OCT-2001; 2001US-00978191.
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PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
XX
PA (GETH) GENENTECH INC.
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PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;

Query Match 100.0%; Score 1685; DB 7; Length 1685;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1685; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 CGCAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCT 120
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Db       1681 AAAAA 1685
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ID   ACA63773 standard; cDNA; 1685 BP.
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DT   16-JUN-2003  (first entry)
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DE   Novel human secreted and transmembrane protein PRO273 cDNA.
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KW   Human; secreted and transmembrane protein; PRO; antiinflammatory;
KW   antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;
KW   antidiabetic; gene therapy; inflammatory disease; organ failure;
KW   atherosclerosis; cardiac injury; infertility; birth defect;
KW   premature aging; AIDS; cancer; diabetic complication; chromosome mapping;
KW   gene mapping; pharmaceutical; diagnostic; biosensor; bioreactor;
KW   tissue typing; gene; ss.
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OS   Homo sapiens.
XX
PN   US2002192706-A1.
XX
PD   19-DEC-2002.
XX
PF   24-OCT-2001; 2001US-00999832.
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PR   09-APR-1998;   98US-0081229P.
PR   15-APR-1998;   98US-0081817P.
PR   15-APR-1998;   98US-0081819P.
PR   15-APR-1998;   98US-0081838P.
PR   15-APR-1998;   98US-0081952P.
PR   15-APR-1998;   98US-0081955P.
PR   21-APR-1998;   98US-0082568P.
PR   21-APR-1998;   98US-0082569P.
PR   22-APR-1998;   98US-0082700P.
PR   22-APR-1998;   98US-0082704P.
PR   22-APR-1998;   98US-0082797P.
PR   22-APR-1998;   98US-0082804P.
PR   23-APR-1998;   98US-0082796P.
PR   07-OCT-1998;   98WO-US021141.
PR   20-NOV-1998;   98WO-US024855.
PR   05-JAN-1999;   99WO-US000106.
PR   08-MAR-1999;   99WO-US005028.
PR   10-MAR-1999;   99WO-US005190.
PR   14-MAY-1999;   99WO-US010733.
PR   02-JUN-1999;   99WO-US012252.
PR   30-NOV-1999;   99WO-US028313.
PR   02-DEC-1999;   99WO-US028551.
PR   02-DEC-1999;   99WO-US028565.
PR   16-DEC-1999;   99WO-US030095.
PR   30-DEC-1999;   99WO-US031243.
PR   30-DEC-1999;   99WO-US031274.
PR   05-JAN-2000; 2000WO-US000219.
PR   06-JAN-2000; 2000WO-US000277.
PR   06-JAN-2000; 2000WO-US000376.
PR   11-FEB-2000; 2000WO-US003565.
PR   18-FEB-2000; 2000WO-US004341.
PR   24-FEB-2000; 2000WO-US005004.
PR   02-MAR-2000; 2000WO-US005841.
PR   10-MAR-2000; 2000WO-US006319.
PR   21-MAR-2000; 2000WO-US007532.
PR   30-MAR-2000; 2000WO-US008439.
PR   17-MAY-2000; 2000WO-US013705.
PR   22-MAY-2000; 2000WO-US014042.
PR   30-MAY-2000; 2000WO-US014941.
PR   02-JUN-2000; 2000WO-US015264.
PR   28-JUL-2000; 2000WO-US020710.
PR   24-AUG-2000; 2000WO-US023328.
PR   01-DEC-2000; 2000WO-US032678.
PR   20-DEC-2000; 2000WO-US034956.
PR   28-FEB-2001; 2001WO-US006520.
PR   22-MAR-2001; 2001WO-US009552.
PR   25-MAY-2001; 2001WO-US017092.
PR   01-JUN-2001; 2001WO-US017800.
PR   20-JUN-2001; 2001WO-US019692.
PR   29-JUN-2001; 2001WO-US021066.
PR   09-JUL-2001; 2001WO-US021735.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Botstein D,  Desnoyers L,  Eaton DL;
PI   Ferrara N,  Filvaroff E,  Fong S,  Gao W,  Gerber H,  Gerritsen ME;
PI   Goddard A,  Godowski PJ,  Grimaldi JC,  Gurney AL,  Hillan KJ;
PI   Kljavin IJ,  Kuo SS,  Napier MA,  Pan J,  Paoni NF,  Roy MA,  Shelton DL;
PI   Stewart TA,  Tumas D,  Williams PM,  Wood WI;
XX
DR   WPI; 2003-328860/31.
DR   P-PSDB; ABU72247.
XX
PT   New secreted and transmembrane nucleic acids and polypeptides, designated
PT   as PRO, useful for treating inflammation, organ failure, atherosclerosis,
PT   cardiac injury, infertility, birth defects, premature aging, AIDS, or
PT   cancer.
XX
PS   Claim 2; Fig 148; 453pp; English.
XX
CC   The invention describes an isolated nucleic acid (I) comprising, or which
CC   is at least 80 % sequence identity to, or the full-length coding sequence
CC   of, any of 118 300-2100 nucleotide sequences, which encodes its
CC   corresponding PRO polypeptide selected from 118 100-700 amino acid
CC   sequences, all given in the specification. The nucleic acids and
CC   polypeptides are useful for treating inflammatory diseases, organ
CC   failure, atherosclerosis, cardiac injury, infertility, birth defects,
CC   premature aging, AIDS, cancer, or diabetic complications. The nucleic
CC   acids are useful as hybridisation probes, in chromosome and gene mapping,
CC   and in generating antisense RNA or DNA. The polypeptides are useful as
CC   pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful
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CC   in tissue typing. This sequence encodes a novel human secreted and
CC   transmembrane PRO polypeptide
XX
SQ   Sequence 1685 BP; 484 A; 435 C; 387 G; 379 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 1685;  DB 7;  Length 1685;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1685;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGG 60

Qy         61 CGCAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGCAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCT 120

Qy        121 GGGTGGCGTCTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGTGGCGTCTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCC 180

Qy        181 ACGCCGCGCCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACGCCGCGCCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCT 240

Qy        241 GGCGCTGTACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAA 300
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Db        241 GGCGCTGTACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAA 300

Qy        301 GATCCGCTACAGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GATCCGCTACAGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGA 360

Qy        361 GAAGATGGTTATCATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCT 420
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Db        361 GAAGATGGTTATCATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCT 420

Qy        421 GCACCCCAAGCTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAA 480
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Db        421 GCACCCCAAGCTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAA 480

Qy        481 GCGCAGGGTCTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTG 540
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Db        481 GCGCAGGGTCTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTG 540

Qy        541 GGAGACTTGTGCAAAGGACTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 600
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Db        541 GGAGACTTGTGCAAAGGACTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 600

Qy        601 AAAAAAAAAAAAAGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGA 660
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Db        601 AAAAAAAAAAAAAGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGA 660

Qy        661 AGCACTTTTTACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGCACTTTTTACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGA 720

Qy        721 TGGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGG 780
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Db        721 TGGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGG 780

Qy        781 GGAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTA 840
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Db        781 GGAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTA 840

Qy        841 TACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTG 900
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Db        841 TACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTG 900

Qy        901 CAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCAC 960
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Db        901 CAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCAC 960

Qy        961 AGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTG 1020
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Db        961 AGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTG 1020

Qy       1021 GCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAA 1080

Qy       1081 GTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGA 1140
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Db       1081 GTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGA 1140

Qy       1141 AACATTTCCAAGATCCTGTGATGGCGAGACAAATGATCCTTAAAGAAGGTGTGGGGTCTT 1200
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Db       1141 AACATTTCCAAGATCCTGTGATGGCGAGACAAATGATCCTTAAAGAAGGTGTGGGGTCTT 1200

Qy       1201 TCCCAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATATTTAATGCTTCAGAAGCATG 1260
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Qy       1261 TGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATATGAATACA 1320
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Qy       1321 TGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGT 1380
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Qy       1441 GTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGATGACCATGCGCCC 1500
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Qy       1501 TTTCCTCTGTACATATACCCTTAAGAACGCCCCCTCCACACACTGCCCCCCCAGTATATGC 1560
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Qy       1561 CGCATTGTACTGCTGTGTTATATGCTATGTACATGTCAGAAACCATTAGCATTGCATGCA 1620
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Qy       1681 AAAAA 1685
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Db       1681 AAAAA 1685
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RESULT 7
ABV72423
ID   ABV72423 standard; cDNA; 1685 BP.
XX
AC   ABV72423;
XX
DT   29-JAN-2003  (first entry)
XX
DE   Nucleotide sequence of Human Bolekine.
XX
KW   Human; Bolekine; T-lymphocyte proliferation; immune related disorder;
KW   systemic lupus erythematosis; rheumatoid arthritis; osteoarthritis;
KW   juvenile chronic arthritis; spondyloarthropathy; systemic sclerosis;
KW   idiopathic inflammatory myopathy; Sjogren's syndrome; gene;
KW   systemic vasculitis; sarcoidosis; autoimmune haemolytic anaemia;
KW   autoimmune thromobocytopaenia; thyroiditis; diabetes mellitus;
KW   immune-mediated renal disease; demyelinating disease;
KW   idiopathic demyelinating polyneuropathy; Guillen-Barre syndrome;
KW   chronic inflammatory demyelinating polyneuropathy; hepatobiliary disease;
KW   hepatitis; primary biliary cirrhosis; granulomatous hepatitis;
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KW   sclerosing cholangitis; inflammatory bowel disease;
KW   gluten-sensitive enteropathy; Whipple's disease; skin disease;
KW   erythema multiforme; contact dermatitis; psoriasis; allergy; asthma;
KW   allergic rhinitis; atopic dermatitis; food hypersensitivity; urticaria;
KW   eosinophilic pneumonia; idiopathic pulmonary fibrosis;
KW   hypersensitivity pneumonitis; graft rejection; graft-versus-host disease;
KW   gene therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             167. .502
FT                   /*tag=  a
FT                   /product= "Bolekine"
FT   sig_peptide     167. .268
FT                   /*tag=  b
XX
PN   WO200277028-A1.
XX
PD   03-OCT-2002.
XX
PF   22-MAR-2001; 2001WO-US009552.
XX
PR   22-MAR-2001; 2001WO-US009552.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Fong S,  Goddard A,  Hillan KJ,  Roth I,  Wood WI;
XX
DR   WPI; 2003-018887/01.
DR   P-PSDB; ABB99340.
XX
PT   New Bolekine polypeptides and encoding nucleic acids, useful for treating
PT   an immune related disorder such as systemic lupus erythematosis,
PT   rheumatoid arthritis, psoriasis, asthma, allergic rhinitis and atopic
PT   dermatitis.
XX
PS   Claim 3; Fig 1; 96pp; English.
XX
CC   The present sequence encodes a human Bolekine polypeptide. Bolekine
CC   polypeptides are active stimulators of the proliferation of T-
CC   lymphocytes. Bolekine polypeptides and polynucleotides are useful for
CC   treating an immune related disorder e.g. systemic lupus erythematosis,
CC   rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, a
CC   spondyloarthropathy, systemic sclerosis, an idiopathic inflammatory
CC   myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis,
CC   autoimmune haemolytic anaemia, autoimmune thromobocytopaenia,
CC   thyroiditis, diabetes mellitus, immune-mediated renal disease, a
CC   demyelinating disease of the central or peripheral nervous system,
CC   idiopathic demyelinating polyneuropathy, Guillen-Barre syndrome, a
CC   chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
CC   disease, infectious or autoimmune chronic active hepatitis, primary
CC   biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
CC   inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
CC   disease, an autoimmune or immune-mediated skin disease, a bullous skin
CC   disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
CC   disease, asthma, allergic rhinitis, atopic dermatitis, food
CC   hypersensitivity, urticaria, an immunologic disease of the lung,
CC   eosinophilic pneumonias, idiopathic pulmonary fibrosis, hypersensitivity
CC   pneumonitis, a transplantation associated disease, graft rejection or
CC   graft-versus-host disease. The Bolekine polypeptides and encoding nucleic
CC   acid molecules can also be used as hybridization probes, for generation
CC   of transgenic animal, gene therapy, as molecular weight markers,
CC   chromosome identification and tissue typing
XX
SQ   Sequence 1685 BP; 484 A; 435 C; 387 G; 379 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 1685;  DB 7;  Length 1685;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1685;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGG 60
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Db          1 GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGG 60

Qy         61 CGCAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCT 120
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Qy        121 GGGTGGCGTCTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCC 180
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Qy        181 ACGCCGCGCCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCT 240
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Db        181 ACGCCGCGCCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCT 240

Qy        241 GGCGCTGTACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAA 300
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Db        241 GGCGCTGTACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAA 300

Qy        301 GATCCGCTACAGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGA 360
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Db        301 GATCCGCTACAGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGA 360

Qy        361 GAAGATGGTTATCATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCT 420
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Qy        421 GCACCCCAAGCTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAA 480
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Db        421 GCACCCCAAGCTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAA 480

Qy        481 GCGCAGGGTCTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCGCAGGGTCTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTG 540

Qy        541 GGAGACTTGTGCAAAGGACTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGAGACTTGTGCAAAGGACTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 600

Qy        601 AAAAAAAAAAAAAGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAAAAAAAAAAAAGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGA 660

Qy        661 AGCACTTTTTACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGA 720
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Db        661 AGCACTTTTTACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGA 720

Qy        721 TGGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTTATCAAAAAGG 780
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Qy        781 GGAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTA 840
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Db        781 GGAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTA 840

Qy        841 TACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTG 900
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Db        841 TACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTG 900

Qy        901 CAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCAC 960
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Qy        961 AGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTG 1020
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Db        961 AGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTG 1020

Qy       1021 GCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAA 1080
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Qy       1081 GTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGA 1140
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Db       1081 GTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGA 1140
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Qy       1141 AACATTTCCAAGATCCTGTGATGGCGAGACAAATGATCCTTAAAGAAGGTGTGGGGTCTT 1200
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Qy       1201 TCCCAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATATTTAATGCTTCAGAAGCATG 1260
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Qy       1261 TGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATATGAATACA 1320
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Db       1261 TGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATATGAATACA 1320

Qy       1321 TGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGT 1380
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Qy       1381 TTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATATTTGTGATTCCCCAT 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATATTTGTGATTCCCCAT 1440

Qy       1441 GTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGATGACCATGCGCCC 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGATGACCATGCGCCC 1500

Qy       1501 TTTCCTCTGTACATATACCCTTAAGAACGCCCCCTCCACACACTGCCCCCCAGTATATGC 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 TTTCCTCTGTACATATACCCTTAAGAACGCCCCCTCCACACACTGCCCCCCAGTATATGC 1560

Qy       1561 CGCATTGTACTGCTGTGTTATATGCTATGTACATGTCAGAAACCATTAGCATTGCATGCA 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CGCATTGTACTGCTGTGTTATATGCTATGTACATGTCAGAAACCATTAGCATTGCATGCA 1620

Qy       1621 GGTTTCATATTCTTTCTAAGATGGAAAGTAATAAAATATATTTGAAATGTAAAAAAAAAA 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GGTTTCATATTCTTTCTAAGATGGAAAGTAATAAAATATATTTGAAATGTAAAAAAAAAA 1680

Qy       1681 AAAAA 1685
             |||||
Db       1681 AAAAA 1685
```

RESULT 8
ACA71937
ID ACA71937 standard; cDNA; 1685 BP.
XX
AC ACA71937;
XX
DT 11-AUG-2003 (first entry)
XX
DE Human secreted and transmembrane PRO polypeptide #3 cDNA.
XX
KW Human; ss; gene; thrombolytic agent; interferon; interleukin; cytokine;
KW erythropoietin; colony stimulating factor; cancer; colorectal carcinoma;
KW apoptosis related condition; AIDS; amyotrophic lateral sclerosis;
KW inflammatory disease; asthma; atherosclerosis; neurodegenerative disease;
KW gastrointestinal disorder; Alzheimer's disease; Parkinson's disease;
KW hypertension; myocardial ischaemia; kidney disease; carcinogenesis;
KW glomerulonephritis; lung disease; pulmonary hypertension; preeclampsia;
KW bronchial asthma; gastric ulcer; renal failure; cardiovascular disease;
KW inflammatory bowel disease; reproductive disorder; premature labour.
XX
OS Homo sapiens.
XX
PN US2002177553-A1.
XX
PD 28-NOV-2002.
XX
PF 15-OCT-2001; 2001US-00978192.
XX
PR 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-00040220.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079294P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 26-JUN-1998; 98US-00105413.
PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98WO-US021141.
PR 02-NOV-1998; 98US-00184216.
PR 06-NOV-1998; 98US-00187368.
PR 20-NOV-1998; 98WO-US024855.
PR 07-DEC-1998; 98US-00202054.
PR 22-DEC-1998; 98US-00218517.
PR 05-JAN-1999; 99WO-US000106.
PR 05-MAR-1999; 99US-00254465.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99US-00265686.
PR 10-MAR-1999; 99WO-US005190.
PR 12-MAR-1999; 99US-00267213.
PR 12-APR-1999; 99US-00284291.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380142.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000US-00709238.
PR 27-NOV-2000; 2000US-00723749.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 22-MAR-2001; 2001US-00816920.
PR 22-MAR-2001; 2001WO-US009552.

PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR WPI; 2003-328499/31.
DR P-PSDB; ABU84927.
XX
PT New isolated PRO polypeptides e.g. PRO213, PRO274 and PRO300, for use as
PT pharmaceuticals, diagnostics, biosensors and bioreactors, for identifying
PT modulators of receptor-ligand interactions.
XX
PS Claim 2; SEQ ID NO 369; 55pp; English.
XX
CC The invention relates to an isolated secreted and transmembrane
CC polypeptide, designated as PRO polypeptide. The PRO polypeptide is useful
CC in PRO polypeptide detection methods. The PRO polypeptide is useful for
CC linking a bioactive molecule to a cell. The PRO polypeptide or an
CC antibody against it is useful for modulating a biological activity of a
CC cell. The PRO polypeptide is useful in industrial applications including
CC pharmaceuticals, diagnostics, biosensors and bioreactors. The PRO
CC polypeptide is also useful as a thrombolytic agent, interferon,
CC interleukin, erythropoietin, colony stimulating factor and other
CC cytokines. The PRO polypeptide is useful for treating disease such as
CC cancer e.g. colorectal carcinoma; apoptosis related conditions e.g. AIDS,
CC amyotrophic lateral sclerosis; inflammatory disease e.g. asthma,
CC atherosclerosis; neurodegenerative disease e.g. Alzheimer's disease,
CC Parkinson's disease; cardiovascular disease e.g. hypertension and
CC myocardial ischaemia; kidney disease e.g. renal failure and
CC glomerulonephritis; lung disease e.g. pulmonary hypertension, bronchial
CC asthma; gastrointestinal disorders e.g. gastric ulcer and inflammatory
CC bowel disease; reproductive disorders e.g. premature labour and
CC preeclampsia; carcinogenesis. The present sequence represents a cDNA
CC encoding a PRO polypeptide of the invention. Note: The sequence data for
CC this patent did not form part of the printed specification but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20020177553
XX
SQ Sequence 1685 BP; 484 A; 435 C; 387 G; 379 T; 0 U; 0 Other;

Query Match 100.0%; Score 1685; DB 7; Length 1685;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1685; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGG 60

Qy         61 CGCAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGCAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCT 120

Qy        121 GGGTGGCGTCTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGTGGCGTCTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCC 180

Qy        181 ACGCCGCGCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACGCCGCGCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCT 240

Qy        241 GGCGCTGTACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGCGCTGTACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAA 300

Qy        301 GATCCGCTACAGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GATCCGCTACAGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGA 360

Qy        361 GAAGATGGTTATCATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAAGATGGTTATCATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCT 420

Qy        421 GCACCCCAAGCTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCACCCCAAGCTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAA 480

Qy        481 GCGCAGGGTCTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCGCAGGGTCTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTG 540

Qy        541 GGAGACTTGTGCAAAGGACTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGAGACTTGTGCAAAGGACTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 600

Qy        601 AAAAAAAAAAAAAGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAAAAAAAAAAAAGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGA 660

Qy        661 AGCACTTTTTACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGCACTTTTTACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGA 720

Qy        721 TGGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGG 780

Qy        781 GGAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GGAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTA 840

Qy        841 TACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTG 900

Qy        901 CAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCAC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCAC 960

Qy        961 AGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTG 1020

Qy       1021 GCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAA 1080

Qy       1081 GTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGA 1140

Qy       1141 AACATTTCCAAGATCCTGTGATGGCGAGACAAATGATCCTTAAAGAAGGTGTGGGGTCTT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AACATTTCCAAGATCCTGTGATGGCGAGACAAATGATCCTTAAAGAAGGTGTGGGGTCTT 1200

Qy       1201 TCCCAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATATTTAATGCTTCAGAAGCATG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TCCCAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATATTTAATGCTTCAGAAGCATG 1260

Qy       1261 TGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATATGAATACA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1261 TGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATATGAATACA 1320

Qy       1321 TGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGT 1380

Qy       1381 TTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATATTTGTGATTCCCCAT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATATTTGTGATTCCCCAT 1440

Qy       1441 GTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGATGACCATGCGCCC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGATGACCATGCGCCC 1500

Qy       1501 TTTCCTCTGTACATATACCCTTAAGAACGCCCCCTCCACACACTGCCCCCCAGTATATGC 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 TTTCCTCTGTACATATACCCTTAAGAACGCCCCCTCCACACACTGCCCCCCAGTATATGC 1560

Qy       1561 CGCATTGTACTGCTGTGTTATATGCTATGTACATGTCAGAAACCATTAGCATTGCATGCA 1620
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Db       1561 CGCATTGTACTGCTGTGTTATATGCTATGTACATGTCAGAAACCATTAGCATTGCATGCA 1620

Qy       1621 GGTTTCATATTCTTTCTAAGATGGAAAGTAATAAAATATATTTGAAATGTAAAAAAAAAA 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GGTTTCATATTCTTTCTAAGATGGAAAGTAATAAAATATATTTGAAATGTAAAAAAAAAA 1680

Qy       1681 AAAAA 1685
              |||||
Db       1681 AAAAA 1685
```

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RESULT 9
ABX92577
ID   ABX92577 standard; cDNA; 1685 BP.
XX
AC   ABX92577;
XX
DT   08-MAY-2003  (first entry)
XX
DE   cDNA encoding human PRO273 polypeptide.
XX
KW   Human; PRO polypeptide; secreted and transmembrane protein;
KW   immune disorder; diabetes; hyper-insulinaemia; hypo-insulinaemia;
KW   cardiac insufficiency; nervous system disorder; kidney disorder;
KW   bone disorder; cartilage disorder; arthritis; tumour; wound healing;
KW   genetic disorder; cytostatic; antidiabetic; antiinflammatory;
KW   antiarthritic; anti-tumour; vulnerary; antianaemic; dermatological;
KW   cardiant; gene; ss.
XX
OS   Homo sapiens.
XX
PN   US2002169284-A1.
XX
PD   14-NOV-2002.
XX
PF   16-OCT-2001; 2001US-00978697.
XX
PR   26-MAY-1981;   81US-00267213.
PR   17-OCT-1997;   97US-0062250P.
PR   03-NOV-1997;   97US-0064249P.
PR   13-NOV-1997;   97US-0065311P.
PR   21-NOV-1997;   97US-0066364P.
PR   10-MAR-1998;   98US-0077450P.
PR   11-MAR-1998;   98US-0077632P.
PR   11-MAR-1998;   98US-0077641P.
PR   11-MAR-1998;   98US-0077649P.
PR   12-MAR-1998;   98US-0077791P.
PR   13-MAR-1998;   98US-0078004P.
PR   17-MAR-1998;   98US-00040220.
PR   20-MAR-1998;   98US-0078886P.
PR   20-MAR-1998;   98US-0078910P.
PR   20-MAR-1998;   98US-0078936P.
PR   20-MAR-1998;   98US-0078939P.
PR   25-MAR-1998;   98US-0079294P.
PR   26-MAR-1998;   98US-0079656P.
PR   27-MAR-1998;   98US-0079663P.
PR   27-MAR-1998;   98US-0079664P.
PR   27-MAR-1998;   98US-0079689P.
PR   27-MAR-1998;   98US-0079728P.
PR   27-MAR-1998;   98US-0079786P.
PR   30-MAR-1998;   98US-0079920P.
PR   30-MAR-1998;   98US-0079923P.
PR   26-JUN-1998;   98US-00105413.
PR   07-OCT-1998;   98US-00168978.
PR   07-OCT-1998;   98WO-US021141.
PR   02-NOV-1998;   98US-00184216.
PR   06-NOV-1998;   98US-00187368.
PR   20-NOV-1998;   98WO-US024855.
PR   07-DEC-1998;   98US-00202054.
PR   22-DEC-1998;   98US-00218517.
PR   05-JAN-1999;   99WO-US000106.
PR   05-MAR-1999;   99US-00254465.
PR   08-MAR-1999;   99WO-US005028.
PR   10-MAR-1999;   99US-00265686.
PR   10-MAR-1999;   99WO-US005190.
PR   12-APR-1999;   99US-00284291.
PR   14-MAY-1999;   99US-00311832.
PR   14-MAY-1999;   99WO-US010733.
PR   02-JUN-1999;   99WO-US012252.
PR   25-AUG-1999;   99US-00380137.
PR   25-AUG-1999;   99US-00380138.
PR   25-AUG-1999;   99US-00380142.
PR   30-NOV-1999;   99WO-US028313.
PR   02-DEC-1999;   99WO-US028551.
PR   02-DEC-1999;   99WO-US028565.
PR   16-DEC-1999;   99WO-US030095.
PR   30-DEC-1999;   99WO-US031243.
PR   30-DEC-1999;   99WO-US031274.
PR   05-JAN-2000; 2000WO-US000219.
PR   06-JAN-2000; 2000WO-US000277.
PR   06-JAN-2000; 2000WO-US000376.
PR   11-FEB-2000; 2000WO-US003565.
PR   18-FEB-2000; 2000WO-US004341.
PR   24-FEB-2000; 2000WO-US005004.
PR   02-MAR-2000; 2000WO-US005841.
PR   10-MAR-2000; 2000WO-US006319.
PR   21-MAR-2000; 2000WO-US007532.
PR   30-MAR-2000; 2000WO-US008439.
PR   17-MAY-2000; 2000WO-US013705.
PR   22-MAY-2000; 2000WO-US014042.
PR   30-MAY-2000; 2000WO-US014941.
PR   02-JUN-2000; 2000WO-US015264.
PR   28-JUL-2000; 2000WO-US020710.
PR   24-AUG-2000; 2000WO-US023328.
PR   08-NOV-2000; 2000US-00709238.
PR   27-NOV-2000; 2000US-00723749.
PR   01-DEC-2000; 2000WO-US032678.
PR   20-DEC-2000; 2000US-00747259.
PR   20-DEC-2000; 2000WO-US034956.
PR   28-FEB-2001; 2001WO-US006520.
PR   22-MAR-2001; 2001US-00816744.
PR   22-MAR-2001; 2001US-00816920.
PR   22-MAR-2001; 2001WO-US009552.
PR   10-MAY-2001; 2001US-00854208.
PR   10-MAY-2001; 2001US-00854280.
PR   25-MAY-2001; 2001WO-US017092.
PR   01-JUN-2001; 2001US-00872035.
PR   01-JUN-2001; 2001WO-US017800.
PR   05-JUN-2001; 2001US-00874503.
PR   14-JUN-2001; 2001US-00882636.
PR   19-JUN-2001; 2001US-00886342.
PR   20-JUN-2001; 2001WO-US019692.
PR   29-JUN-2001; 2001WO-US021066.
PR   09-JUL-2001; 2001WO-US021735.
PR   30-JUL-2001; 2001US-00918585.
XX
```

PA (GETH) GENENTECH INC.
XX
PI Ashkenazi A, Baker KP, Botstein D, Desnoyers L, Eaton D;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR WPI; 2003-288163/28.
DR P-PSDB; ABU61125.
XX
PT Novel secreted and transmembrane polypeptides and polynucleotides
PT encoding them useful for treating cancer, kidney diseases, bone,
PT cartilage disorders and immune deficiencies.
XX
PS Claim 2; Fig 148; 459pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for linking
CC bioactive molecules to cells expressing PRO polypeptides, for modulating
CC biological activities of cells expressing PRO polypeptides, and for for
CC identifying agonists or antagonists. The bioactive molecule maybe a
CC toxin, radiolabel or antibody, and causes apoptosis or death of the cell.
CC The PRO polypeptides are useful for treating immune disorders, diabetes
CC or hyper- or hypo-insulinaemia, cardiac insufficiency, nervous system
CC disorders, kidney disorders, bone and cartilage disorders or arthritis,
CC tumours, and wound healing. The polynucleotide sequences encoding PRO
CC polypeptides are useful as hybridisation probes, in chromosome and gene
CC mapping, in the generation of antisense RNA and DNA, in the preparation
CC of PRO polypeptides, for generating transgenic animals or knockout
CC animals, for the genetic analysis of individuals with genetic disorders,
CC and in gene therapy. The present sequence encodes a human PRO polypeptide
CC of the invention. Note: The sequence data for this patent was obtained in
CC electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/psipsDIDEntry.html
XX
SQ Sequence 1685 BP; 484 A; 435 C; 387 G; 379 T; 0 U; 0 Other;

Query Match 100.0%; Score 1685; DB 7; Length 1685;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1685; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGG 60
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Db          1 GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGG 60

Qy         61 CGCAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGCAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCT 120

Qy        121 GGGTGGCGTCTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGTGGCGTCTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCC 180

Qy        181 ACGCCGCGCCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACGCCGCGCCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCT 240

Qy        241 GGCGCTGTACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGCGCTGTACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAA 300

Qy        301 GATCCGCTACAGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GATCCGCTACAGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGA 360

Qy        361 GAAGATGGTTATCATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAAGATGGTTATCATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCT 420

Qy        421 GCACCCCAAGCTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAA 480
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Db        421 GCACCCCAAGCTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAA 480

Qy        481 GCGCAGGGTCTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTG 540
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Db        481 GCGCAGGGTCTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTG 540

Qy        541 GGAGACTTGTGCAAAGGACTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGAGACTTGTGCAAAGGACTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 600

Qy        601 AAAAAAAAAAAAAAGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGA 660
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Db        601 AAAAAAAAAAAAAAGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGA 660

Qy        661 AGCACTTTTTACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGA 720
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Db        661 AGCACTTTTTACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGA 720

Qy        721 TGGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGG 780

Qy        781 GGAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GGAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTA 840

Qy        841 TACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTG 900

Qy        901 CAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCAC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCAC 960

Qy        961 AGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTG 1020
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Db        961 AGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTG 1020

Qy       1021 GCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAA 1080
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Db       1021 GCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAA 1080

Qy       1081 GTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGA 1140
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Db       1081 GTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGA 1140

Qy       1141 AACATTTCCAAGATCCTGTGATGGCGAGACAAATGATCCTTAAAGAAGGTGTGGGGTCTT 1200
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Db       1141 AACATTTCCAAGATCCTGTGATGGCGAGACAAATGATCCTTAAAGAAGGTGTGGGGTCTT 1200

Qy       1201 TCCCAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATATTTAATGCTTCAGAAGCATG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TCCCAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATATTTAATGCTTCAGAAGCATG 1260

Qy       1261 TGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATATGAATACA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATATGAATACA 1320

Qy       1321 TGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGT 1380

Qy       1381 TTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATATTTGTGATTCCCCAT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATATTTGTGATTCCCCAT 1440

Qy       1441 GTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGATGACCATGCGCCC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGATGACCATGCGCCC 1500

Qy       1501 TTTCCTCTGTACATATACCCTTAAGAACGCCCCCTCCACACACTGCCCCCCAGTATATGC 1560
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Db       1501 TTTCCTCTGTACATATACCCTTAAGAACGCCCCCTCCACACACTGCCCCCCAGTATATGC 1560

Qy       1561 CGCATTGTACTGCTGTGTTATATGCTATGTACATGTCAGAAACCATTAGCATTGCATGCA 1620
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Db       1561 CGCATTGTACTGCTGTGTTATATGCTATGTACATGTCAGAAACCATTAGCATTGCATGCA 1620

Qy       1621 GGTTTCATATTCTTTCTAAGATGGAAAGTAATAAAATATATTTGAAATGTAAAAAAAAAA 1680
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Db       1621 GGTTTCATATTCTTTCTAAGATGGAAAGTAATAAAATATATTTGAAATGTAAAAAAAAAA 1680

Qy       1681 AAAAA 1685
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Db       1681 AAAAA 1685


RESULT 10
ACA66318
ID   ACA66318 standard; cDNA; 1685 BP.
XX
AC   ACA66318;
XX
DT   24-JUN-2003  (first entry)
XX
DE   Human cDNA encoding secreted/transmembrane protein PRO273.
XX
KW   Human; ss; gene; secreted protein; transmembrane protein; PRO;
KW   malignancy; cancer; ovarian cancer; colorectal cancer; sarcoma;
KW   leukaemia; lymphoma; inflammatory disease; necrosis; atherosclerosis;
KW   infertility; premature aging; psoriasis; inflammatory disease;
KW   renal disease; arthritis; immune-mediated alopecia; stroke; encephalitis;
KW   hepatitis; multiple sclerosis; gene therapy.
XX
OS   Homo sapiens.
XX
PN   US2003004102-A1.
XX
PD   02-JAN-2003.
XX
PF   15-OCT-2001; 2001US-00978189.
XX
PR   17-OCT-1997;   97US-0062250P.
PR   03-NOV-1997;   97US-0064249P.
PR   13-NOV-1997;   97US-0065311P.
PR   21-NOV-1997;   97US-0066364P.
PR   10-MAR-1998;   98US-0077450P.
PR   11-MAR-1998;   98US-0077632P.
PR   11-MAR-1998;   98US-0077641P.
PR   11-MAR-1998;   98US-0077649P.
PR   12-MAR-1998;   98US-0077791P.
PR   13-MAR-1998;   98US-0078004P.
PR   17-MAR-1998;   98US-00040220.
PR   20-MAR-1998;   98US-0078886P.
PR   20-MAR-1998;   98US-0078910P.
PR   20-MAR-1998;   98US-0078936P.
PR   20-MAR-1998;   98US-0078939P.
PR   25-MAR-1998;   98US-0079294P.
PR   26-MAR-1998;   98US-0079656P.
PR   27-MAR-1998;   98US-0079663P.
PR   27-MAR-1998;   98US-0079664P.
PR   27-MAR-1998;   98US-0079689P.
PR   27-MAR-1998;   98US-0079728P.
PR   27-MAR-1998;   98US-0079786P.
PR   30-MAR-1998;   98US-0079920P.
PR   30-MAR-1998;   98US-0079923P.
PR   26-JUN-1998;   98US-00105413.
PR   07-OCT-1998;   98US-00168978.
PR   07-OCT-1998;   98WO-US021141.
PR   02-NOV-1998;   98US-00184216.
PR   06-NOV-1998;   98US-00187368.
PR   20-NOV-1998;   98WO-US024855.
PR   07-DEC-1998;   98US-00202054.
PR   22-DEC-1998;   98US-00218517.
PR   05-JAN-1999;   99WO-US000106.
PR   05-MAR-1999;   99US-00254465.
PR   08-MAR-1999;   99WO-US005028.
PR   10-MAR-1999;   99US-00265686.
PR   10-MAR-1999;   99WO-US005190.
PR   12-MAR-1999;   99US-00267213.
PR   12-APR-1999;   99US-00284291.
PR   14-MAY-1999;   99US-00311832.
PR   14-MAY-1999;   99WO-US010733.
PR   02-JUN-1999;   99WO-US012252.
PR   25-AUG-1999;   99US-00380137.
PR   25-AUG-1999;   99US-00380138.
PR   25-AUG-1999;   99US-00380142.
PR   30-NOV-1999;   99WO-US028313.
PR   02-DEC-1999;   99WO-US028551.
PR   02-DEC-1999;   99WO-US028565.
PR   16-DEC-1999;   99WO-US030095.
PR   30-DEC-1999;   99WO-US031243.
PR   30-DEC-1999;   99WO-US031274.
PR   05-JAN-2000; 2000WO-US000219.
PR   06-JAN-2000; 2000WO-US000277.
PR   06-JAN-2000; 2000WO-US000376.
PR   11-FEB-2000; 2000WO-US003565.
PR   18-FEB-2000; 2000WO-US004341.
PR   24-FEB-2000; 2000WO-US005004.
PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005841.
PR   10-MAR-2000; 2000WO-US006319.
PR   21-MAR-2000; 2000WO-US007532.
PR   30-MAR-2000; 2000WO-US008439.
PR   17-MAY-2000; 2000WO-US013705.
PR   22-MAY-2000; 2000WO-US014042.
PR   30-MAY-2000; 2000WO-US014941.
PR   02-JUN-2000; 2000WO-US015264.
PR   28-JUL-2000; 2000WO-US020710.
PR   24-AUG-2000; 2000WO-US023328.
PR   08-NOV-2000; 2000US-00709238.
PR   10-NOV-2000; 2000WO-US030873.
PR   27-NOV-2000; 2000US-00723749.
PR   01-DEC-2000; 2000WO-US032678.
PR   20-DEC-2000; 2000US-00747259.
PR   20-DEC-2000; 2000WO-US034956.
PR   28-FEB-2001; 2001WO-US006520.
PR   22-MAR-2001; 2001US-00816744.
PR   22-MAR-2001; 2001US-00816920.
PR   22-MAR-2001; 2001WO-US009552.
PR   10-MAY-2001; 2001US-00854208.
PR   10-MAY-2001; 2001US-00854280.
PR   25-MAY-2001; 2001WO-US017092.
PR   01-JUN-2001; 2001US-00872035.
PR   01-JUN-2001; 2001WO-US017800.
PR   05-JUN-2001; 2001US-00874503.
PR   14-JUN-2001; 2001US-00882636.
PR   19-JUN-2001; 2001US-00886342.
PR   20-JUN-2001; 2001WO-US019692.
PR   29-JUN-2001; 2001WO-US021066.
PR   09-JUL-2001; 2001WO-US021735.
PR   30-JUL-2001; 2001US-00918585.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Botstein D,  Desnoyers L,  Eaton DL;
PI   Ferrara N,  Filvaroff E,  Fong S,  Gao W,  Gerber H,  Gerritsen ME;
PI   Goddard A,  Godowski PJ,  Grimaldi JC,  Gurney AL,  Hillan KJ;
PI   Kljavin IJ,  Kuo SS,  Napier MA,  Pan J,  Paoni NF,  Roy MA,  Shelton DL;
PI   Stewart TA,  Tumas D,  Williams PM,  Wood WI;
XX
DR   WPI; 2003-341189/32.
DR   P-PSDB; ABU80394.
XX
PT   New genes and secreted and transmembrane polypeptides (e.g. PRO337 or
PT   PRO1559), useful for treating or diagnosing e.g. cancers,
PT   atherosclerosis, infertility, stroke, encephalitis, hepatitis or multiple
PT   sclerosis in mammals.
```

XX
PS Claim 2; Fig 148; 460pp; English.
XX
CC The invention relates to a new isolated nucleic acid molecule comprises a
CC sequence with at least 80% identity to: (a) a nucleotide encoding any of
CC 94 PRO polypeptides whose sequences are fully defined in the
CC specification; or (b) any of 94 nucleotide sequences fully defined in the
CC specification; or the full length coding sequence of any these 94
CC nucleotide sequences. Also included are an isolated PRO polypeptide
CC scoring at least 80% positives when compared to any of the PRO
CC polypeptide sequences cited above (or an isolated PRO polypeptide having
CC at least 80% amino acid sequence identity to: (a) an amino acid sequence
CC encoded by the nucleotide deposited with ATCC numbers listed in the
CC specification; (b) the PRO polypeptide, lacking its associated signal
CC peptide; or (c) an extracellular domain of the PRO polypeptide, with or
CC lacking its associated signal peptide), a vector comprising the nucleic
CC acid molecule, a host cell comprising the vector (and producing a PRO
CC polypeptide), a chimaeric molecule comprising the PRO polypeptide fused
CC to a heterologous amino acid sequence and an anti-PRO antibody. The PRO
CC polypeptides or polynucleotides are useful as pharmaceuticals,
CC diagnostics, biosensors or bioreactors. These are particularly useful for
CC detecting or treating e.g. malignancies or cancers (e.g. ovarian cancer,
CC colorectal cancer, sarcoma, leukaemia or lymphoma), inflammatory disease,
CC necrosis, atherosclerosis, infertility, premature aging, psoriasis,
CC inflammatory disease, renal disease, arthritis, immune-mediated alopecia,
CC stroke, encephalitis, hepatitis, or multiple sclerosis in mammals. The
CC PRO polypeptides are useful in drug screening, particularly as targets
CC for therapeutic intervention in these diseases, and in the diagnostic
CC determination of the presence of these diseases. The PRO polypeptides are
CC also useful as molecular weight markers, or for chromosome
CC identification. The PRO genes are useful as hybridisation probes, or for
CC screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may
CC also be used in gene therapy, particularly for replacing a defective
CC gene. The present sequence encodes a PRO polypeptide
XX
SQ Sequence 1685 BP; 484 A; 435 C; 387 G; 379 T; 0 U; 0 Other;

Query Match 100.0%; Score 1685; DB 7; Length 1685;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1685; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGG 60

Qy         61 CGCAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCT 120
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Db         61 CGCAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCT 120

Qy        121 GGGTGGCGTCTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGTGGCGTCTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCC 180

Qy        181 ACGCCGCGCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACGCCGCGCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCT 240

Qy        241 GGCGCTGTACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGCGCTGTACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAA 300

Qy        301 GATCCGCTACAGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GATCCGCTACAGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGA 360

Qy        361 GAAGATGGTTATCATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAAGATGGTTATCATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCT 420

Qy        421 GCACCCCAAGCTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAA 480
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Qy        481 GCGCAGGGTCTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTG 540
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Qy        601 AAAAAAAAAAAAAGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGA 660
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Qy        661 AGCACTTTTTACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGCACTTTTTACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGA 720

Qy        721 TGGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGG 780
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Db        721 TGGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGG 780

Qy        781 GGAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GGAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTA 840

Qy        841 TACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTG 900

Qy        901 CAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCAC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCAC 960

Qy        961 AGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTG 1020

Qy       1021 GCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAA 1080

Qy       1081 GTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGA 1140
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Db       1081 GTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGA 1140

Qy       1141 AACATTTCCAAGATCCTGTGATGGCGAGACAAATGATCCTTAAAGAAGGTGTGGGGTCTT 1200
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Qy       1201 TCCCAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATATTTAATGCTTCAGAAGCATG 1260
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Db       1201 TCCCAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATATTTAATGCTTCAGAAGCATG 1260

Qy       1261 TGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATATGAATACA 1320
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Db       1261 TGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATATGAATACA 1320

Qy       1321 TGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGT 1380
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Db       1321 TGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGT 1380

Qy       1381 TTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATATTTGTGATTCCCCAT 1440
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Db       1381 TTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATATTTGTGATTCCCCAT 1440

Qy       1441 GTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGATGACCATGCGCCC 1500
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Qy       1561 CGCATTGTACTGCTGTGTTTATATGCTATGTACATGTCAGAAACCATTAGCATTGCATGCA 1620
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Qy       1681 AAAAA 1685
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Db       1681 AAAAA 1685


RESULT 11
ADA24908
ID   ADA24908 standard; cDNA; 1685 BP.
XX
AC   ADA24908;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO273 cDNA.
XX
KW   Human; secreted and transmembrane protein; PRO; gene; ss; tissue typing;
KW   chromosome identification; vaccine; cancer; retinal disorder;
KW   sports-related joint disorder; osteoarthritis; rheumatoid arthritis;
KW   wound healing; obesity; diabetes; hearing loss;
KW   cardiac insufficiency disorder; kidney disorder; nervous system disorder;
KW   haemoglobin associated disorder.
XX
OS   Homo sapiens.
XX
PN   US2003050241-A1.
XX
PD   13-MAR-2003.
XX
PF   16-OCT-2001; 2001US-00978564.
XX
PR   17-OCT-1997;   97US-0062250P.
PR   03-NOV-1997;   97US-0064249P.
PR   13-NOV-1997;   97US-0065311P.
PR   21-NOV-1997;   97US-0066364P.
PR   10-MAR-1998;   98US-0077450P.
PR   11-MAR-1998;   98US-0077632P.
PR   11-MAR-1998;   98US-0077641P.
PR   11-MAR-1998;   98US-0077649P.
PR   12-MAR-1998;   98US-0077791P.
PR   13-MAR-1998;   98US-0078004P.
PR   20-MAR-1998;   98US-0078886P.
PR   20-MAR-1998;   98US-0078910P.
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PR   20-MAR-1998;   98US-0078939P.
PR   25-MAR-1998;   98US-0079294P.
PR   26-MAR-1998;   98US-0079656P.
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PR   14-MAY-1999;   99US-0134287P.
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PR   06-JAN-2000; 2000WO-US000277.
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PR   11-FEB-2000; 2000WO-US003565.
PR   18-FEB-2000; 2000WO-US004341.
PR   24-FEB-2000; 2000WO-US005004.
PR   02-MAR-2000; 2000WO-US005841.
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PR   01-JUN-2001; 2001WO-US017800.
PR   20-JUN-2001; 2001WO-US019692.
PR   29-JUN-2001; 2001WO-US021066.
PR   09-JUL-2001; 2001WO-US021735.
PR   30-JUL-2001; 2001US-00918585.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Botstein D,  Desnoyers L,  Eaton DL;
PI   Ferrara N,  Filvaroff E,  Fong S,  Gao W,  Gerber H,  Gerritsen ME;
PI   Goddard A,  Godowski PJ,  Grimaldi JC,  Gurney AL,  Hillan KJ;
PI   Kljavin IJ,  Kuo SS,  Napier MA,  Pan J,  Paoni NF,  Roy MA,  Shelton DL;
PI   Stewart TA,  Tumas D,  Williams PM,  Wood WI;
XX
DR   WPI; 2003-521814/49.
DR   P-PSDB; ADA24909.
XX
PT   New isolated PRO polypeptides for example extracellular, secreted and
PT   membrane bound proteins, useful for modulating the biological activities
PT   of cells and for treating, for example diabetes, cancer, rheumatoid
PT   arthritis, and hearing loss.
XX
PS   Claim 2; Fig 148; 461pp; English.
XX
CC   The invention describes an isolated secreted and transmembrane (PRO)
CC   polypeptide (I). PRO337 polypeptide is useful for detecting PRO4993
CC   polypeptide in a sample, and vice versa. PRO725, PRO700 and PRO739 are
CC   useful for detecting PRO1559 polypeptide in a sample, and PRO1559 is
CC   useful for detecting PRO725, PRO700 and PRO739 in a sample. PRO4993 is
CC   useful for linking a bioactive molecule to a cell expressing a PRO337
CC   polypeptide, and PRO337 is useful for linking a bioactive molecule to a
CC   cell expressing a PRO4993 polypeptide. PRO1559 is useful for linking a
CC   bioactive molecule to a cell expressing a PRO735, PRO700 and PRO739

  Query Match           100.0%;  Score 1685;  DB 8;  Length 1685;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1685;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         61 CGCAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCT 120
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Db         61 CGCAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCT 120

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Qy        181 ACGCCGCGCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        301 GATCCGCTACAGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGA 360
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Qy        361 GAAGATGGTTATCATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCT 420
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Qy        421 GCACCCCAAGCTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAA 480
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Qy        481 GCGCAGGGTCTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTG 540
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Qy        541 GGAGACTTGTGCAAAGGACTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 600
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Db        541 GGAGACTTGTGCAAAGGACTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 600

Qy        601 AAAAAAAAAAAAAGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGA 660
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Qy        661 AGCACTTTTTACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGA 720
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Qy        721 TGGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGG 780
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Qy        781 GGAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTA 840
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Qy        841 TACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTG 900
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Qy        901 CAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCAC 960
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Qy        961 AGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTG 1020
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Qy       1021 GCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAA 1080
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Db       1021 GCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAA 1080

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Db       1081 GTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGA 1140

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Db       1681 AAAAA 1685
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RESULT 12
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ID ACD29919 standard; cDNA; 1685 BP.
XX
AC ACD29919;
XX
DT 08-SEP-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO273 cDNA.
XX
KW Human; secreted and transmembrane protein; PRO; cell death; neuropathy;
KW peripheral neuropathy; diabetic peripheral neuropathy;
KW AIDS-associated neuropathy; Charcot-Marie-Tooth disease;
KW Refusum's disease; Abetalipoproteinaemia; Tangier disease;
KW Krabbe's disease; Metachromatic leukodystrophy; Fabry's disease;
KW Dejerine-Sottas syndrome; chromosome mapping; gene mapping; gene therapy;
KW gene; ss.
XX
OS Homo sapiens.
XX
PN US2003050240-A1.
XX
PD 13-MAR-2003.
XX
PF 16-OCT-2001; 2001US-00978403.
XX
PR 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066364P.
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PR 31-MAR-1998; 98US-0080165P.
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PR 30-JUL-2001; 2001US-00918585.

XX
PA (GETH) GENENTECH INC.
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PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WL;
XX
DR WPI; 2003-503575/47.
DR P-PSDB; ABO19696.
XX
PT Novel secreted and transmembrane polypeptide for modulating biological
PT activity of cell expressing the polypeptide, identifying agonists or
PT antagonists of polypeptide, and as molecular weight markers.
XX
PS Claim 2; Fig 148; 459pp; English.
XX
CC The invention describes an isolated, secreted and transmembrane
CC polypeptide, termed PRO polypeptide (I). (I) is useful for detecting
CC PRO4993, PRO337, PRO1559, PRO725, PRO700 or PRO739 polypeptide, and for
CC linking a bioactive molecule to a cell expressing the above polypeptides.
CC The bioactive molecule is a toxin, radiolabel or an antibody and causes
CC cell death. (I) is useful as therapeutic agent, in medical and industrial
CC applications e.g. for treating neuropathy, especially peripheral
CC neuropathy, diabetic peripheral neuropathy, AIDS-associated neuropathy,
CC Charcot-Marie-Tooth disease, Refusum's disease, Abetalipoproteinaemia,

Query Match 100.0%; Score 1685; DB 8; Length 1685;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1685; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       1681 AAAAA 1685
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ID ADA12569 standard; cDNA; 1685 BP.
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AC ADA12569;
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DT 06-NOV-2003 (first entry)
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DE Human cDNA encoding secreted/transmembrane polypeptide PRO273.
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KW ss; gene; inflammatory disease; organ failure; atherosclerosis;
KW cardiac injury; infertility; birth defect; premature aging; AIDS; cancer;
KW diabetic complication; tissue typing; human.
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OS Homo sapiens.
XX
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PD 20-MAR-2003.
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XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;

Query Match 100.0%; Score 1685; DB 8; Length 1685;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1685; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       121 GGGTGGCGTCTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCC 180
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Qy       901 CAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCAC 960
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Qy       961 AGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTG 1020
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Qy      1081 GTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGA 1140
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Qy      1441 GTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGATGACCATGCGCCC 1500
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Db      1681 AAAAA 1685
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RESULT 14
ACD29334
ID ACD29334 standard; cDNA; 1685 BP.
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AC ACD29334;
XX
DT 27-AUG-2003 (first entry)
XX
DE Novel human secreted and transmembrane polypeptide cDNA #94.
XX
KW Human; secreted and transmembrane protein; PRO; viral infection;
KW tumour growth; retinal disorder; injury; sight loss;
KW retinitis pigmentosum; age-related macular degeneration;
KW sport-related joint problem; articular cartilage defect; osteoarthritis;
KW rheumatoid arthritis; wound healing; obesity; diabetes; insulinaemia;
KW kidney disorder; mesangial cell function; Berger disease; nephropathy;
KW celiac disease; dermatitis; Crohn disease; neuropathy;
KW cardiac- insufficiency disorder; peripheral neuropathy;
KW diabetic peripheral neuropathy; autonomic neuropathy;
KW reduced motility of the gastrointestinal tract;
KW atony of the urinary bladder; post polio syndrome; Krabbe's disease;
KW Charcot-Marie-Tooth disease; Fabry's disease; Tangier disease;
KW Refsum's disease; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003049633-A1.
XX
PD 13-MAR-2003.
XX
PF 16-OCT-2001; 2001US-00978585.
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PR 05-JAN-2000; 2000WO-US000219.
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PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.

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PR   08-NOV-2000; 2000US-00709238.
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PR   01-DEC-2000; 2000WO-US032678.
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PR   14-JUN-2001; 2001US-00882636.

  Query Match           100.0%;  Score 1685;  DB 8;  Length 1685;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1685;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        121 GGGTGGCGTCTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCC 180
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Qy        661 AGCACTTTTTTACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGA 720
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RESULT 15
ADB73875
ID   ADB73875 standard; cDNA; 1685 BP.
XX
AC   ADB73875;
XX
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DT 04-DEC-2003 (first entry)
XX
DE Human PRO polynucleotide sequence #94.
XX
KW Human; PRO polypeptide; secreted protein; transmembrane protein;
KW cell death; neuropathy; neuropathy related disease;
KW Charcot-Marie-Tooth disorder; Refsum's disease; Krabbe's disease;
KW chromosome mapping; gene mapping; genetic disorder; septic shock;
KW antibacterial; immunosuppressive; neuroprotective; gene; ss.
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OS Homo sapiens.
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PN US2003045462-A1.
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PD 06-MAR-2003.
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PA   (GETH ) GENENTECH INC.
XX

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Job time : 711 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 26, 2004, 05:10:44 ; Search time 4581 Seconds
(without alignments)
10984.015 Million cell updates/sec

Title: US-09-978-189-369
Perfect score: 1685
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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22: em_gss_mam:*
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28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	4	839.2	49.8	953	9	AL543855	AL543855 AL543855
	5	835	49.6	858	12	BG696197	BG696197 602659321
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	8	805.4	47.8	829	12	BG677521	BG677521 602625161
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	31	618.6	36.7	707	12	BG619277	BG619277 602619402
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c	45	587	34.8	595	12	BM669121	BM669121 UI-E-DW0-

ALIGNMENTS

RESULT 1
BM809019
LOCUS BM809019 1019 bp mRNA linear EST 05-MAR-2002
DEFINITION AGENCOURT_6618019 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5734462 5', mRNA sequence.
ACCESSION BM809019
VERSION BM809019.1 GI:19125842
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1019)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12739 row: m column: 23
High quality sequence stop: 661.

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FEATURES             Location/Qualifiers
     source          1. .1019
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5734462"
                     /tissue_type="hippocampus"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_124"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: EcoRV
                     (destroyed); Site_2: NotI; RNA source male hippocampus,
                     age 27. Library is oligo-dT primed and directionally
                     cloned (EcoRV site is destroyed upon cloning). Average
                     insert size 1.4 kb, insert size range 0.9-4 kb. Library is
                     normalized and enriched for full-length clones and was
                     constructed by C. Gruber (Invitrogen). Research Genetics
                     tracking code 012."
ORIGIN

  Query Match           53.1%;  Score 895;  DB 12;  Length 1019;
  Best Local Similarity  95.5%;  Pred. No. 3.3e-120;
  Matches  942;  Conservative    0;  Mismatches   41;  Indels    3;  Gaps    2;

Qy        619 TCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGAAGCACTTTTTACCAACGG 678
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         11 TCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGAAGCACTTTTTACCAACGG 70

Qy        679 TCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGATGGGAGACCCATCTCTCT 738
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         71 TCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGATGGGAGACCCATCTCTCT 130

Qy        739 TGTGCTCCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGGGGAAAACTCATGCCTTTC 798
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        131 TGTGCTCCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGGGGAAAACTCATGCCTTTC 190

Qy        799 CTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTATACATCTGAGCTTTATAA 858
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 CTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTATACATCTGAGCTTTATAA 250

Qy        859 GCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTGCAGTGTTGCTCCATTCCT 918
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 GCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTGCAGTGTTGCTCCATTCCT 310

Qy        919 AGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCACAGCTGCCACGGGCTCTCC 978
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 AGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCACAGCTGCCACGGGCTCTCC 370

Qy        979 TGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTGGCCCCTGTAGCCGGGCAA 1038
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Db        371 TGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTGGCCCCTGTAGCCGGGCAA 430

Qy       1039 GCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAAGTTTGGTTGCCAGAAAAA 1098
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        431 GCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAAGTTTGGTTGCCAGAAAAA 490

Qy       1099 TGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGAAACATTTCCAAGATCCTG 1158
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        491 TGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGAAACATTTCCAAGATCCTG 550

Qy       1159 TGATGGCGAGACAAATGATCCTTAAAGAAGGTGTGGGGTCTTTCCCAACCTGAGGATTTC 1218
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        551 TGATGGCGAGACAAATGATCCTTAAAGAAGGTGTGGGGTCTTTCCCAACCTGAGGATTTC 610

Qy       1219 TGAAAGGTTCACAGGTTCAATATTTAATGCTTCAGAAGCATGTGAGGTTCCCAACACTGT 1278
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Db        611 TGAAAGGTTCACAGGTTCAATATTTAATGCTTCAGAAGCATGTGAGGTTCCCAACACTGT 670

Qy       1279 CAGCAAAAACCTTAGGAGAAAACTTAAAAATATATGAATACATGCGCAATACACAGCTAC 1338
              ||||||||||||| |||||||||| ||||||||||||||||||||||||||||||||||||
Db        671 CAGCAAAAACCTTAAGAGAAAACTTANAAATATATGAATACATGCGCAATACACAGCTAC 730

Qy       1339 AGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGTTTCTTTCCCTCACCACAA 1398
              |||||||||||||||||||||||||||||||||||||||||||||||||||     |||||
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Db        731 AGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGTTTCTTTCCCCTCACACAA 790

Qy       1399 CAGAACATGCAGTACTAAAGCAATATATTTGTGATTCCCCATGTAATTCTTCAATGTTAA 1458
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        791 CAGAACATGCAGTACTAAAGCAATATATTTGTGATTCCCCATGTAATTCCTCAATGTTAA 850

Qy       1459 ACAGTGCAGTCCTCTTTCGAAAGCTAAGATGACCATGCG-CCCTTTCCTCTGTACATATA 1517
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Db        851 ACAGTGCAGTCCTCTTTCAAAAGCTAAGATGACCATGCGCCCCTTTCCTCTGTACATATA 910

Qy       1518 CCCTTAAGAACGCCCCC--TCCACACACTGCCCCCCAGTATATGCCGCATTGTACTGCTG 1575
              ||| | | |||||||||  || | | |  |||||||| |||||||     |   |  |||
Db        911 CCCCTTAAAACGCCCCCCTTCAAAAAATGGCCCCCCAGAATATGCCCGCATTGGCACCTG 970

Qy       1576 TGTTATATGCTATGTACATGTCAGAA 1601
                    |  ||||   |||  | ||
Db        971 CTGGGGGTTATATGCCTATGGTACAA 996


RESULT 2
CA975881
LOCUS       CA975881                916 bp    mRNA    linear   EST 06-JAN-2003
DEFINITION  AGENCOURT_8954747 Lupski_sciatic_nerve Homo sapiens cDNA clone
            IMAGE:6202274 5', mRNA sequence.
ACCESSION   CA975881
VERSION     CA975881.1  GI:27508535
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 916)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. James R. Lupski
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13620  row: b  column: 03
            High quality sequence stop: 685.
FEATURES             Location/Qualifiers
     source          1. .916
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6202274"
                     /sex="male"
                     /tissue_type="sciatic nerve"
                     /dev_stage="adult, 70 yr"
                     /lab_host="DH10B"
                     /clone_lib="Lupski_sciatic_nerve"
                     /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
                     NotI; Site_2: SalI; cDNA made by oligo-dT priming.
                     Directionally cloned using the following adaptors:
                     5'-TCGACCCACGCGTCCG-3' and
                     5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'. Size selected >
                     1 kb for average insert length 1.87 kb. This is a primary
                     library, non-amplified. Library constructed by Life
                     Technologies and donated  by J. Lupski, M.D./Ph.D. (Baylor
                     College of Medicine) and is available through Life
                     Technologies."
ORIGIN

  Query Match           52.8%;  Score 890.2;  DB 14;  Length 916;
  Best Local Similarity  98.9%;  Pred. No. 1.7e-119;
  Matches  906;  Conservative    0;  Mismatches    9;  Indels    1;  Gaps    1;
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Qy        684 TTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGATGGGAGACCCATCTCTCTTGTGC 743
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGATGGGAGACCCATCTCTCTTGTGC 60

Qy        744 TCCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGGGGAAAACTCATGCCTTTCCTTTT 803
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGGGGAAAACTCATGCCTTTCCTTTT 120

Qy        804 TAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTATACATCTGAGCTTTATAAGCGCC 863
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTATACATCTGAGCTTTATAAGCGCC 180

Qy        864 CGGGAGGAACAATGAGCTTGGTGGACACATTTCATTGCAGTGTTGCTCCATTCCTAGCTT 923
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Db        181 CGGGAGGAACAATGAGCTTGGTGGACACATTTCATTGCAGTGTTGCTCCATTCCTAGCTT 240

Qy        924 GGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCACAGCTGCCACGGGCTCTCCTGGGC 983
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCACAGCTGCCACGGGCTCTCCTGGGC 300

Qy        984 TTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTGGCCCCTGTAGCCGGGCAAGCAGG 1043
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTGGCCCCTGTAGCCGGGCAAGCAGG 360

Qy       1044 AGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAAGTTTGGTTGCCAGAAAAATGTGC 1103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAAGTTTGGTTGCCAGAAAAATGTGC 420

Qy       1104 TTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGAAACATTTCCAAGATCCTGTGATG 1163
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGAAACATTTCCAAGATCCTGTGATG 480

Qy       1164 GCGAGACAAATGATCCTTAAAGAAGGTGTGGGGTCTTTCCCAACCTGAGGATTTCTGAAA 1223
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCGAGACAAATGATCCTTAAAGAAGGTGTGGGGTCTTTCCCAACCTGAGGATTTCTGAAA 540

Qy       1224 GGTTCACAGGTTCAATATTTAATGCTTCAGAAGCATGTGAGGTTCCCAACACTGTCAGCA 1283
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGTTCACAGGTTCAATATTTAATGCTTCAGAAGCATGTGAGGTTCCCAACACTGTCAGCA 600

Qy       1284 AAAACCTTAGGAGAAAACTTAAAAATATATGAATACATGCGCAATACACAGCTACAGACA 1343
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAAACCTTAGGAGAAAACTTAAAAATATATGAATACATGCGCAATACACAGCTACAGACA 660

Qy       1344 CACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGTTTCTTTCCCTCACCACAACAGAA 1403
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGTTTCTTTCCCTCACCACAACAGAA 720

Qy       1404 CATGCAGTACTAAAGCAATATATTTGTGATTCCCCATGTAATTCTTCAATGTTAAACAGT 1463
              |||||||||||| |||||||||||||||||||||||||||||| ||||||||||||||||
Db        721 CATGCAGTACTANAGCAATATATTTGTGATTCCCCATGTAATTCTTTCATGTTAAACAGT 780

Qy       1464 GCAGTCCTCTTTCGAAAGCTAAGATGACCATGCG-CCCTTTCCTCTGTACATATACCCTT 1522
              |||||||||||||||||||||||||||||||||| |||||||||||||||||||||| |
Db        781 GCAGTCCTCTTTCGAAAGCTAAGATGACCATGCGCCCCTTTCCTCTGTACATATACCCCT 840

Qy       1523 AAGAACGCCCCCTCCACACACTGCCCCCCAGTATATGCCGCATTGTACTGCTGTGTTATA 1582
              ||||| |||||| |||||||||||||||||||||||||||||| ||||||| ||||||
Db        841 AAGAAAGCCCCCCTCACACACTGCCCCCCAGTATATGCCGCATTGGACTGCTGGGTTATA 900

Qy       1583 TGCTATGTACATGTCA 1598
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Db        901 TGCTATGTACATGTCA 916
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RESULT 3
BG678414
LOCUS       BG678414                976 bp    mRNA    linear   EST 01-MAY-2001
DEFINITION  6026250062F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4750214 5',
            mRNA sequence.
ACCESSION   BG678414
VERSION     BG678414.1  GI:13909811
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 976)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Cleaver, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10604  row: k  column: 15
            High quality sequence stop: 864.
FEATURES             Location/Qualifiers
     source          1. .976
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4750214"
                     /tissue_type="squamous cell carcinoma"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NCI_CGAP_Skn4"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.5kb.  Library  constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
ORIGIN
```

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  Query Match           50.2%;  Score 846.4;  DB 12;  Length 976;
  Best Local Similarity   97.7%;  Pred. No. 3.6e-113;
  Matches  891;  Conservative    0;  Mismatches   16;  Indels    5;  Gaps    3;

Qy        616 CTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGAAGCACTTTTTACCAA 675
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGAAGCACTTTTTACCAA 60

Qy        676 CGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGATGGGAGACCCATCTC 735
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGATGGGAGACCCATCTC 120

Qy        736 TCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGGGGAAAACTCATGCCT 795
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGGGGAAAACTCATGCCT 180

Qy        796 TTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTATACATCTGAGCTTTA 855
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Db        181 TTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTATACATCTGAGCTTTA 240

Qy        856 TAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTGCAGTGTTGCTCCATT 915
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Db        241 TAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTGCAGTGTTGCTCCATT 300

Qy        916 CCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCACAGCTGCCACGGGCTC 975
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Db        301 CCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCACAGCTGCCACGGGCTC 360

Qy        976 TCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTGGCCCCTGTAGCCGGG 1035
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Db        361 TCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTGGCCCCTGTAGCCGGG 420

Qy       1036 CAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAAGTTTGGTTGCCAGAA 1095
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Db        421 CAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAAGTTTGGTTGCCAGAA 480

Qy       1096 AAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGAAACATTTCCAAGATC 1155
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Db        481 AAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGAAACATTTCCAAGATC 540
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Qy       1156 CTGTGATGGCGAGACAAATGATCCTTAAAGAAGGTGTGGGGTCTTTCCCAACCTGAGGAT 1215
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGTGATGGCGAGACAAATGATCCTTAAAGAAGGTGTGGGGTCTTTCCCAACCTGAGGAT 600

Qy       1216 TTCTGAAAGGTTCACAGGTTCAATATTTAATGCTTCAGAAGCATGTGAGGTTCCCAACAC 1275
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTCTGAAAGGTTCACAGGTTCAATATTTAATGCTTCAGAAGCATGTGAGGTTCCCAACAC 660

Qy       1276 TGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATATGAATACATGCGCAATACACAGC 1335
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Db        661 TGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATATGAATACATGCGCAATACACAGC 720

Qy       1336 TACAGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGTTTCTTTCCCTCACCA 1395
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        721 TACAGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGTTTCTTTCCCTCA-CA 779

Qy       1396 CAACAGAACATGCAGTACTAAAGCAATATATTTGTGATTCCCCATGTAATTCTTCAATGT 1455
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Db        780 TAACAGAACATGCAGTACTAAAGCAATATTATTGTGATTCCCCATGTAATTCTTCAACTG 839

Qy       1456 TAAACAGTG---CAGTCCTCTTTCG-AAAGCTAAGATGACCATGCGCCCTTTCCTCTGTA 1511
              | |     |   ||||||||||||| ||||||||||  ||||||||||||||||||||
Db        840 TTACACCAGTGCCAGTCCTCTTTCGAAAAGCTAAGATGGACATGCGCCCTTTCCTCTGTA 899

Qy       1512 CATATACCCTTA 1523
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Db        900 CATATTACCTTA 911
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RESULT 4
AL543855
LOCUS       AL543855                953 bp    mRNA    linear   EST 31-MAY-2003
DEFINITION  AL543855 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI005YI22 5-PRIME, mRNA sequence.
ACCESSION   AL543855
VERSION     AL543855.2  GI:31265700
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 953)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 15, 2001 this sequence version replaced gi:12876334.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 3123.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI005BE11QP1&cluster=3123.r. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI005BE11QP1.
FEATURES             Location/Qualifiers
     source          1. .953
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI005YI22"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
```

```
  Query Match           49.8%;  Score 839.2;  DB 9;  Length 953;
  Best Local Similarity  96.6%;  Pred. No. 4e-112;
  Matches  862;  Conservative   22;  Mismatches    5;  Indels    3;  Gaps    3;

Qy        707 GAAAGGCTTCCAGATGGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCT 766
              | | |||||||||||||||||:|||||||||||||||:|:|||||||||||||||||||||
Db         62 GGATGGCTTCCAGATGGGAGASCCATCTCTCTTGTGSTMCAGACTTCATCACAGGCTGCT 121

Qy        767 TTTTATCAAAAAGGGGAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTG 826
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 TTTTATCAAAAAGGGGAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTG 181

Qy        827 TCCATACGTCACTATACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTG 886
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 TCCATACGTCACTATACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTG 241

Qy        887 GACACAT-TTCATTGCAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTC 945
              ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 GACACATATTCATTGCAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTC 301

Qy        946 CTGGCGCCTCGGCACAGCTGCCACGGGCTCT-CCTGGGCTTATGGCCGGTCACAGCCTCA 1004
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        302 CTGGCGCCTCGGCACAGCTGCCACGGGCTCTACCTGGGCTTATGGCCGGTCACAGCCTCA 361

Qy       1005 GT-GTGACTCCACAGTGGCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTG 1063
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 GTAGTGACTCCACAGTGGCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTG 421

Qy       1064 TTCTCTGAGGAACTCAAGTTTGGTTGCCAGAAAAAATGTGCTTCATTCCCCCCTGGTTAAT 1123
              |||||||||||||||||||||||||||:|:|||||||::  | |||||:|:||||||||||
Db        422 TTCTCTGAGGAACTCAAGTTTGGTTGCYARAAAAATGWRAATAATTCCMCMCTGGTTAAT 481

Qy       1124 TTTTACACACCCTAGGAAACATTTCCAAGATCCTGTGATGGCGAGACAAATGATCCTTAA 1183
              |||||||||||||||||||||||:|||||||||||||||||:||:|||||||||||||||||
Db        482 TTTTACACACCCTAGGAAACATTTMCAAGATCCTGTGATGGMGARACAAATGATCCTTAA 541

Qy       1184 AGAAGGTGTGGGGTCTTTCCCAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATATTT 1243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 AGAAGGTGTGGGGTCTTTCCCAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATATTT 601

Qy       1244 AATGCTTCAGAAGCATGTGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTT 1303
              |||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 AATGCTTCARAAGCATGTGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTT 661

Qy       1304 AAAAATATATGAATACATGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGA 1363
              |||||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||
Db        662 AAAAATATATGAATAMATGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGA 721

Qy       1364 AAACCTTCAAAGCATGTTTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATA 1423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        722 AAACCTTCAAAGCATGTTTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATA 781

Qy       1424 TATTTGTGATTCCCCATGTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCT 1483
              |||||||||||||||||||||||||||||||||||||:|||||||||||:|||||||||||
Db        782 TATTTGTGATTCCCCATGTAATTCTTCAATGTTAAAMAGTGCAGTCCTCWTTCGAAAGCT 841

Qy       1484 AAGATGACCATGCGCCCTTTCCTCTGTACATATACCCTTAAGAACGCCCCCTCCACACAC 1543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:
Db        842 AAGATGACCATGCGCCCTTTCCTCTGTACATATACCCTTAAGAACGCCCCCTCCACACAM 901

Qy       1544 TGCCCCCCAGTATATGCCGCATTGTACTGCTGTGTTATATGCTATGTACATG 1595
              |||||||||||||||:|||||||:|||||||||||||:|:||||||:|||
Db        902 TGCCCCCCAGTATATGCMGCATTGTAMTGCTGTGTTATAWGMTATGTAMATG 953
```

```
RESULT 5
BG696197
LOCUS       BG696197                858 bp    mRNA    linear   EST 07-MAY-2001
DEFINITION  602659321F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4802404 5',
            mRNA sequence.
ACCESSION   BG696197
VERSION     BG696197.1  GI:13961096
KEYWORDS    EST.
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```
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 858)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Cleaver, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
            Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10696  row: j  column: 05
            High quality sequence stop: 852.
FEATURES             Location/Qualifiers
     source          1. .858
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4802404"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NCI_CGAP_Skn3"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.5kb.  Library constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
ORIGIN

  Query Match             49.6%;  Score 835;  DB 12;  Length 858;
  Best Local Similarity   99.8%;  Pred. No. 1.7e-111;
  Matches  857;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    2;

Qy        662 GCACTTTTTACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGAT 721
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCACTTTTTACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGAT 60

Qy        722 GGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGGG 781
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGGG 120

Qy        782 GAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTAT 841
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTAT 180

Qy        842 ACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTGC 901
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTGC 240

Qy        902 AGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCACA 961
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCACA 300

Qy        962 GCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTGG 1021
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTGG 360

Qy       1022 CCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAAG 1081
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAAG 420

Qy       1082 TTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGAA 1141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGAA 480

Qy       1142 ACATTTCCAAGATCCTGTGATGGCGAGACAAATGATCCTTAAAGAAGGTGTGGGGTCTTT 1201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ACATTTCCAAGATCCTGTGATGGCGAGACAAATGATCCTTAAAGAAGGTGTGGGGTCTTT 540

Qy       1202 CCCAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATATTTAATGCTTCAGAAGCATGT 1261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCCAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATATTTAATGCTTCAGAAGCATGT 600

Qy       1262 GAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATATGAATACAT 1321
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATATGAATACAT 660

Qy       1322 GCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGTT 1381
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGTT 720

Qy       1382 TCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATATTTGTGATTCCCCATG 1441
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        721 TCTTTCCCTCACCA-AACAGAACATGCAGTACTAAAGCAATATATTTGTGATTCCCCATG 779

Qy       1442 TAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGATGACCATGCG-CCC 1500
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        780 TAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGATGACCATGCGCCCC 839

Qy       1501 TTTCCTCTGTACATATACC 1519
              ||||||||||||||||||
Db        840 TTTCCTCTGTACATATACC 858
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RESULT 6
BQ716973
LOCUS       BQ716973                851 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8241306 Lupski_sympathetic_trunk Homo sapiens cDNA clone
            IMAGE:6187072 5', mRNA sequence.
ACCESSION   BQ716973
VERSION     BQ716973.1  GI:21855870
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 851)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. James R. Lupski
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13580  row: h  column: 17
            High quality sequence stop: 667.
FEATURES             Location/Qualifiers
     source          1. .851
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6187072"
                     /sex="male"
                     /tissue_type="sympathetic trunk"
                     /dev_stage="adult, 16 yr"
                     /lab_host="DH10B"
                     /clone_lib="Lupski_sympathetic_trunk"
                     /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
                     NotI; Site_2: SalI; cDNA made by oligo-dT priming.
                     Directionally cloned using the following adaptors:
                     5'-TCGACCCACGCGTCCG-3' and
                     5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'. Size selected >
                     1 kb for average insert length 1.9 kb. This is a primary
                     library, non-amplified. Library constructed by Life
                     Technologies and donated  by J. Lupski, M.D./Ph.D. (Baylor
                     College of Medicine); available through Life
                     Technologies."
```

ORIGIN

Query Match 48.1%; Score 809.8; DB 13; Length 851;
Best Local Similarity 99.0%; Pred. No. 7.6e-108;
Matches 825; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

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Qy        854 TATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTGCAGTGTTGCTCCA 913
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTGCAGTGTTGCTCCA 60

Qy        914 TTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCACAGCTGCCACGGGC 973
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCACAGCTGCCACGGGC 120

Qy        974 TCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTGGCCCCTGTAGCCG 1033
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTGGCCCCTGTAGCCG 180

Qy       1034 GGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAAGTTTGGTTGCCAG 1093
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAAGTTTGGTTGCCAG 240

Qy       1094 AAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGAAACATTTCCAAGA 1153
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        241 AAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACGCCCTAGGAAACATTTCCAAGA 300

Qy       1154 TCCTGTGATGGCGAGACAAATGATCCTTAAAGAAGGTGTGGGGTCTTTCCCAACCTGAGG 1213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCTGTGATGGCGAGACAAATGATCCTTAAAGAAGGTGTGGGGTCTTTCCCAACCTGAGG 360

Qy       1214 ATTTCTGAAAGGTTCACAGGTTCAATATTTAATGCTTCAGAAGCATGTGAGGTTCCCAAC 1273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATTTCTGAAAGGTTCACAGGTTCAATATTTAATGCTTCAGAAGCATGTGAGGTTCCCAAC 420

Qy       1274 ACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATATGAATACATGCGCAATACACA 1333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATATGAATACATGCGCAATACACA 480

Qy       1334 GCTACAGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGTTTCTTTCCCTCAC 1393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCTACAGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGTTTCTTTCCCTCAC 540

Qy       1394 CACAACAGAACATGCAGTACTAAAGCAATATATTTGTGATTCCCCATGTAATTCTTCAAT 1453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CACAACAGAACATGCAGTACTAAAGCAATATATTTGTGATTCCCCATGTAATTCTTCAAT 600

Qy       1454 GTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGATGACCATGCGCCCTTTCCTCTGTACA 1513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGATGACCATGCGCCCTTTCCTCTGTACA 660

Qy       1514 TATA-CCCTTAAGAACGCCCCCTCCACACACTGCCCCCCAGTATATGCCGCATTGTACTG 1572
              |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TATACCCCTTAAGAACGCCCCCTCCACACACTGCCCCCCAGTATATGCCGCATTGTACTG 720

Qy       1573 CTGTGTTATATGCTATGTACATGTCAGAAACCATTAGCATTGCATGCAGGTTTCATATTC 1632
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTGTGTTATATGCTATGTACATGTCAGAAACCATTAGCATTGCATGCAGGTTTCATATTC 780

Qy       1633 TTTCTAAGATGGAAAGTAATAAAATATATTTGAAATGTAAAAAAAAAAAAAAA 1685
              |||||||||||||||||||||||||||||||  ||   ||||||||||||||
Db        781 TTTCTAAGATGGAAAGTAATAAAATATATTTTGAAATGTAAAAAAAAAAAAAA 833
```

RESULT 7
AL570175/c
LOCUS AL570175 937 bp mRNA linear EST 31-MAY-2003
DEFINITION AL570175 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI005YI22 3-PRIME, mRNA sequence.
ACCESSION AL570175
VERSION AL570175.2 GI:31291600
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 937)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 16, 2001 this sequence version replaced gi:12926227.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 3123.r For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI005BE11NP1&cluster=3123.r. Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0DI005BE11NP1.
FEATURES Location/Qualifiers
source 1. .937
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI005YI22"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 47.8%; Score 805.8; DB 9; Length 937;
Best Local Similarity 93.6%; Pred. No. 2.8e-107;
Matches 860; Conservative 26; Mismatches 27; Indels 6; Gaps 5;

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Qy        723 GGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGGGG 782
              ||||||||||:|||:|:: |||||| ||||||||||||||::|||| :||||:|||
Db        932 GGAGACCCATYTCTYTKK-GCTCCATACTTCATCACAGGCTRYTTTT--ATMAAAARGGG 876

Qy        783 AAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTATA 842
              |||||:||::|||||||||||||||||||||||||||||||||||||||||||||||||
Db        875 AAAACWCAWRCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTATA 816

Qy        843 CATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTGCA 902
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||:|||
Db        815 CATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGAACACATTTCATWGCA 756

Qy        903 GTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCACAG 962
              |||||||||||| ||||||||||||||||||||||||||||||:||||||:|||| ||||
Db        755 GTGTTGCTCCATACCTAGCTTGGGAAGCTTCCGCTTAGAGGTCYTGGCGCYTCGGAACAG 696

Qy        963 CTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTGGC 1022
              :|||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||
Db        695 MTGCCACGGGYTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTGGC 636

Qy       1023 CCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAAGT 1082
              |||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||
Db        635 CCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTMTGAGGAACTCAAGT 576

Qy       1083 TTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGAAA 1142
              |||||||||||||||||||||||| |||||||||||||||| ||||||||||||||||
Db        575 TTGGTTGCCAGAAAAATGTGCTTCATACCCCCCTGGTTAATTTTAACACACCCTAGGAAA 516

Qy       1143 CATTTCCAAGATCCTGTGATGGCGAGACAAATGATCCTTAAAGAAGGTGTGGGGTCTTTC 1202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        515 CATTTCCAAGATCCTGTGATGGCGAGACAAATGATCCTTAAAGAAGGTGTGGGGTCTTTC 456

Qy       1203 CCAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATATTTAA-TGCTTCAGAAGCATGT 1261
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        455 CCAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATATTTAACTGCTTCAGAAGCATGT 396
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Qy       1262 GAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATATGAATACAT 1321
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        395 GAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATATGAATACAT 336

Qy       1322 GCGCAATACACAGCTACAGACACACAT-TCTGTTGACAAGGGAAAACCTTCAAAGCATGT 1380
             ||||||||||||||||||||:|||||| |||||||:|||||||||||||||||||||||||
Db        335 GCGCAATACACAGCTACAGAMACACATATCTGTTGMCAAGGGAAAACCTTCAAAGCATGT 276

Qy       1381 TTCTTTCCCTCACCACAACAGAACATGCAG-TACTAAAGCAATATATTTGTGATTCCCCA 1439
             |||||||||||||||||||||||||||||| :|||||||||||||||||||||||||||||
Db        275 TTCTTTCCCTCACCACAACAGAACATGCAGAWACTAAAGCAATATATTTGTGATTCCCCA 216

Qy       1440 TGTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGATGACCATGCGCC 1499
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        215 TGTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGATGACCATGCGCC 156

Qy       1500 CTTTCCTCTGTACATATACCCTTAAGAACGCCCCCTCCACACACTGCCCCCCAGTATATG 1559
             ||||||||||||||||||||||||||||||::|||||:|||||||||||| |:||||
Db        155 CTTTCCTCTGTACATATACCCTTAAGAACGCCCMYTCCACMCACTGCCCCCCGGGYATATA 96

Qy       1560 CCGCATTGTACTGCTGTGTTATATGCTATGTACATGTCAGAAACCATTAGCATTGCATGC 1619
             |||||||| |||:|||||||||||||||||||||||||||    || |  |  :|||||||||
Db          95 CCGCATTGNACTKCTGTGTTATATGCTATGTACATGTACAGAAACCATTASATTGCATGC 36

Qy       1620 AGGTTTCATATTCTTTCTA 1638
              |||||| | |  ||  ||
Db         35 NGGTTTCNTNTCTTTCTTA 17


RESULT 8
BG677521
LOCUS       BG677521                829 bp    mRNA    linear   EST 01-MAY-2001
DEFINITION  602625161F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4750167 5',
            mRNA sequence.
ACCESSION   BG677521
VERSION     BG677521.1  GI:13908918
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 829)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Cleaver, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10604  row: i  column: 16
            High quality sequence stop: 827.
FEATURES             Location/Qualifiers
     source          1. .829
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4750167"
                     /tissue_type="squamous cell carcinoma"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NCI_CGAP_Skn4"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.5kb.  Library  constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
ORIGIN

  Query Match             47.8%;  Score 805.4;  DB 12;  Length 829;
  Best Local Similarity   99.6%;  Pred. No. 3.3e-107;

  Matches  828;  Conservative    0;  Mismatches    1;  Indels    2;  Gaps    2;

Qy        654 GTTATGAAGCACTTTTTACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGC 713
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTTATGAAGCACTTTTTACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGC 60

Qy        714 TTCCAGATGGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTATC 773
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTCCAGATGGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTATC 120

Qy        774 AAAAAGGGGAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATAC 833
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAAAAGGGGAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATAC 180

Qy        834 GTCACTATACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACAT 893
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTCACTATACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACAT 240

Qy        894 TTCATTGCAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCC 953
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TTCATTGCAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCC 300

Qy        954 TCGGCACAGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTC 1013
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCGGCACAGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTC 360

Qy       1014 CACAGTGGCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGG 1073
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Db        361 CACAGTGGCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGG 420

Qy       1074 AACTCAAGTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACAC 1133
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AACTCAAGTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACAC 480

Qy       1134 CCTAGGAAACATTTCCAAGATCCTGTGATGGCGAGACAAATGATCCTTAAAGAAGGTGTG 1193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCTAGGAAACATTTCCAAGATCCTGTGATGGCGAGACAAATGATCCTTAAAGAAGGTGTG 540

Qy       1194 GGGTCTTTCCCAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATATTTAATGCTTCAG 1253
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGGTCTTTCCCAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATATTTAATGCTTCAG 600

Qy       1254 AAGCATGTGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATAT 1313
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Db        601 AAGCATGTGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATAT 660

Qy       1314 GAATACATGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACCTTCAA 1373
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Db        661 GAATACATGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACCTTCAA 720

Qy       1374 AGCATGTTTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATATTTGTGAT 1433
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        721 AGCATGTTTCTTTCCCTCACCA-AACAGAACATGCAGTACTAAAGCAATATATTTGTGAT 779

Qy       1434 TCCCCATGTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTA 1484
              |||||||| |||||||||||| ||||||||||||||||||||||||||||
Db        780 TCCCCATGTTATTCTTCAATGTT-AACAGTGCAGTCCTCTTTCGAAAGCTA 829


RESULT 9
BG679254
LOCUS       BG679254                844 bp    mRNA    linear   EST 01-MAY-2001
DEFINITION  602627337F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4752104 5',
            mRNA sequence.
ACCESSION   BG679254
VERSION     BG679254.1  GI:13910651
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 844)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
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  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Cleaver, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10609  row: j  column: 09
            High quality sequence stop: 839.
FEATURES             Location/Qualifiers
     source          1. .844
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4752104"
                     /tissue_type="squamous cell carcinoma"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NCI_CGAP_Skn4"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.5kb.  Library  constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
ORIGIN

  Query Match             47.5%;  Score 800;  DB 12;  Length 844;
  Best Local Similarity   98.7%;  Pred. No. 2e-106;
  Matches  838;  Conservative    0;  Mismatches    6;  Indels    5;  Gaps    3;

Qy        711 GGCTTCCAGATGGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTT 770
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGCTTCCAGATGGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTT 60

Qy        771 ATCAAAAAGGGGAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCA 830
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCAAAAAGGGGAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCA 120

Qy        831 TACGTCACTATACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACA 890
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TACGTCACTATACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACA 180

Qy        891 CATTTCATTGCAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGC 950
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CATTTCATTGCAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGC 240

Qy        951 GCCTCGGCACAGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGA 1010
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCCTCGGCACAGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGA 300

Qy       1011 CTCCACAGTGGCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTG 1070
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTCCACAGTGGCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTG 360

Qy       1071 AGGAACTCAAGTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACA 1130
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Db        361 AGGAACTCAAGTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACA 420

Qy       1131 CACCCTAGGAAACATTTCCAAGATCCTGTGATGGCGAGACAAATGATCCTTAAAGAAGGT 1190
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Db        421 CACCCTAGGAAACATTTCCAAGATCCTGTGATGGCGAGACAAATGATCCTTAAAGAAGGT 480

Qy       1191 GTGGGGTCTTTCCCAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATATTTAATGCTT 1250
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Db        481 GTGGGGTCTTTCCCAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATATTTAATGCTT 540

Qy       1251 CAGAAGCATGTGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATA 1310
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CAGAAGCATGTGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATA 600

Qy       1311 TATGAATACATGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACCTT 1370
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TATGAATACATGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACCTT 660

Qy       1371 CAAAGCATGTTTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATATTTGT 1430
              ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        661 CAAAGCATGTTTCTTTCCCTCACCANAACAGAACATGCAGTACTAAAGCAATATATTTGT 720

Qy       1431 GATTCCCCATGTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGATGA 1490
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GATTCCCCATGTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGATGA 780

Qy       1491 CCATGCGCCCTTTCCTCTGTACATATACCCTTAAGAACGCCCCCTCCACACACTGCCCCC 1550
              |||||||||||||||||||||||  ||||||||||||||  | |||   || ||||
Db        781 -CATGCGCCCTTTCCTCTGTACATAT-TCCTTAAGAACGCCCCTCCAACA---TGACCCC 835

Qy       1551 CAGTATATG 1559
              |||||||||
Db        836 CAGTATATG 844


RESULT 10
BQ889304
LOCUS       BQ889304                 817 bp    mRNA    linear   EST 16-AUG-2002
DEFINITION  AGENCOURT_8482592 Lupski_dorsal_root_ganglion Homo sapiens cDNA
            clone IMAGE:6185842 5', mRNA sequence.
ACCESSION   BQ889304
VERSION     BQ889304.1  GI:22281318
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 817)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. James R. Lupski
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13577  row: e  column: 11
            High quality sequence stop: 587.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6185842"
                     /sex="male"
                     /tissue_type="dorsal root ganglia"
                     /dev_stage="adult, 36 yr"
                     /lab_host="DH10B"
                     /clone_lib="Lupski_dorsal_root_ganglion"
                     /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
                     NotI; Site_2: SalI; cDNA made by oligo-dT priming.
                     Directionally cloned using the following adaptors:
                     5'-TCGACCCACGCGTCCG-3' and
                     5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'. Size selected >
                     1 kb for average insert length 1.7 kb. This is a primary
                     library, non-amplified. Library constructed by Life
                     Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
                     College of Medicine) and is available through Life
                     Technologies."
ORIGIN

  Query Match             47.3%;  Score 796.8;  DB 13;  Length 817;
  Best Local Similarity   98.8%;  Pred. No. 5.8e-106;
  Matches  801;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;
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Qy        875 ATGAGCTTGGTGGACACATTTCATTGCAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCC 934
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 ATGAGCTTGGTGGACACATTTCATTGCAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCC 64

Qy        935 GCTTAGAGGTCCTGGCGCCTCGGCACAGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGT 994
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         65 GCTTAGAGGTCCTGGCGCCTCGGCACAGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGT 124

Qy        995 CACAGCCTCAGTGTGACTCCACAGTGGCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCT 1054
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        125 CACAGCCTCAGTGTGACTCCGCAGTGGCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCT 184

Qy       1055 CTGCATCTGTTCTCTGAGGAACTCAAGTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCC 1114
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 CTGCATCTGTTCTCTGAGGAACTCAAGTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCC 244

Qy       1115 CTGGTTAATTTTTACACACCCTAGGAAACATTTCCAAGATCCTGTGATGGCGAGACAAAT 1174
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Qy       1175 GATCCTTAAAGAAGGTGTGGGGTCTTTCCCAACCTGAGGATTTCTGAAAGGTTCACAGGT 1234
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Db        305 GATCCTTAAAGAAGGTGTGGGGTCTTTCCCAACCTGAGGATTTCTGAAAGGTTCACAGGT 364

Qy       1235 TCAATATTTAATGCTTCAGAAGCATGTGAGGTTCCCAACACTGTCAGCAAAAACCTTAGG 1294
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Db        365 TCAATATTTAATGCTTCAGAAGCATGTGAGGTTCCCAACACTGTCAGCAAAAACCTTAGG 424

Qy       1295 AGAAAACTTAAAAATATATGAATACATGCGCAATACACAGCTACAGACACACATTCTGTT 1354
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        425 AGAAAACTTAAAAATATATGAATACATGCGCAATACACAGCTACAGACACACATTCTGTT 484

Qy       1355 GACAAGGGAAAACCTTCAAAGCATGTTTCTTTCCCTCACCACAACAGAACATGCAGTACT 1414
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Db        485 GACAAGGGAAAACCTTCAAAGCATGTTTCTTTCCCTCACCACAACAGAACATGCAGTACT 544

Qy       1415 AAAGCAATATATTTGTGATTCCCCATGTAATTCTTCAATGTTAAACAGTGCAGTCCTCTT 1474
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Db        545 AAAGCAATATATTTGTGATTCCCCATGTAATTCTTCAATGTTAAACAGTGCAGTCCTCTT 604

Qy       1475 TCGAAAGCTAAGATGACCATGCGCCCTTTCCTCTGTACATATACCCTTAAGAACGCCCCC 1534
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Qy       1535 TCCACACACTGCCCCCCAGTATATGCCGCATTGTACTGCTGTGTTATATGCTATGTACAT 1594
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Qy       1595 GTCAGAAACCATTAGCATTGCATGCAGGTTTCATATTCTTTCTAAGATGGAAAGTAATAA 1654
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Db        725 GTCAGAANACATTAGCATTGCATGCAGGTTTCATATTCTTTCNTAGATGGAAAGNTATAA 784

Qy       1655 AATATATTTGAAATGTAAAAAAAAAAAAAAA 1685
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Db        785 AATATATTTGAAATGTAAAAAAAAAAAAAAA 815
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RESULT 11
BG677005
LOCUS       BG677005                794 bp    mRNA    linear   EST 01-MAY-2001
DEFINITION  602623644F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4748603 5',
            mRNA sequence.
ACCESSION   BG677005
VERSION     BG677005.1  GI:13908402
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 794)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Cleaver, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10600  row: h  column: 12
            High quality sequence stop: 787.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /clone="IMAGE:4748603"
                     /tissue_type="squamous cell carcinoma"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NCI_CGAP_Skn4"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.5kb.  Library  constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
ORIGIN
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Query Match 45.1%; Score 759.2; DB 12; Length 794;
Best Local Similarity 98.9%; Pred. No. 1.6e-100;
Matches 775; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTTATGAAGCACTTTTTACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGC 60

Qy        714 TTCCAGATGGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTATC 773
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTCCAGATGGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTATC 120

Qy        774 AAAAAGGGGAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATAC 833
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAAAAGGGGAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATAC 180

Qy        834 GTCACTATACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACAT 893
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTCACTATACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACAT 240

Qy        894 TTCATTGCAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCC 953
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TTCATTGCAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCC 300

Qy        954 TCGGCACAGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTC 1013
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCGGCACAGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTC 360

Qy       1014 CACAGTGGCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGG 1073
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CACAGTGGCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGG 420

Qy       1074 AACTCAAGTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACAC 1133
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AACTCAAGTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACAC 480

Qy       1134 CCTAGGAAACATTTCCAAGATCCTGTGATGGCGAGACAAATGATCCTTAAAGAAGGTGTG 1193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCTAGGAAACATTTCCAAGATCCTGTGATGGCGAGACAAATGATCCTTAAAGAAGGTGTG 540

Qy       1194 GGGTCTTTCCCAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATATTTAATGCTTCAG 1253
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGGTCTTTCCCAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATATTTAATGCTTCAG 600

Qy       1254 AAGCATGTGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATAT 1313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
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Db        601 AAGCATGTGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATAT-T 659

Qy       1314 GAATACATGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACCTTCAA 1373

Db        660 GAATACATGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACCTTCAA 719

Qy       1374 AGCATGTTTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATATTTGTGAT 1433

Db        720 AGCATGTTTCTTTCCCCTCACCACAAAGAACATGCAGTACTAAAGCAATATATTTGTGAT 779

Qy       1434 TCCC 1437

Db        780 TCCC 783
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RESULT 12
BG679890
LOCUS       BG679890                 860 bp    mRNA    linear   EST 01-MAY-2001
DEFINITION  602626393F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4751327 5',
            mRNA sequence.
ACCESSION   BG679890
VERSION     BG679890.1  GI:13911287
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 860)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Cleaver, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10607  row: i  column: 24
            High quality sequence stop: 858.
FEATURES             Location/Qualifiers
     source          1. .860
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4751327"
                     /tissue_type="squamous cell carcinoma"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NCI_CGAP_Skn4"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.5kb.  Library  constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
ORIGIN
```

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  Query Match             44.8%;  Score 754.4;  DB 12;  Length 860;
  Best Local Similarity   97.3%;  Pred. No. 7.9e-100;
  Matches  831;  Conservative    0;  Mismatches   16;  Indels    7;  Gaps    6;

Qy        637 GACACAAATTATATATTGTTATGAAGCACTTTTTACCAACGGTCAGTTTTTACATTTTAT 696

Db          1 GACACAAATTATATATTGTTATGAAGCACTTTTTACCAACGGTCAGTTTTTACATTTTAT 60

Qy        697 AGCTGCGTGCGAAAGGCTTCCAGATGGGAGACCCATCTCTCTTGTGCTCCAGACTTCATC 756

Db         61 AGCTGCGTGCGAAAGGCTTCCAGATGGGAGACCCATCTCTCTTGTGCTCCAGACTTCATC 120

Qy        757 ACAGGCTGCTTTTTTATCAAAAAGGGGAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTT 816

Db        121 ACAGGCTGCTTTTTTATCAAAAAGGGGAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTT 180

Qy        817 TTT-GTATTTGTCCATACGTCACTATACATCTGAGCTTTATAAGCGCCCGGGAGGAACAA 875

Db        181 TTTGGTATTTGTCCATACGTCACTATACATCTGAGCTTTATAAGCGCCCGGGAGGAACAA 240

Qy        876 TGAGCTTGGTGGACACATTTCATTGCAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCG 935

Db        241 TGAGCTTGGTGGACACATTTCATTGCAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCG 300

Qy        936 CTTAGAGGTCCTGGCGCCTCGGCACAGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTC 995

Db        301 CTTAGAGGTCCTGGCGCCTCGGCACAGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTC 360

Qy        996 ACAGCCTCAGTGTGACTCCACAGTGGCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTC 1055

Db        361 ACAGCCTCAGTGTGACTCCACAGTGGCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTC 420

Qy       1056 TGCATCTGTTCTCTGAGGAACTCAAGTTTGGTTGCCAGAAAA--ATGTGCTTCATTCCCC 1113

Db        421 TGCATCTGTTCTCTGAGGAACTCAAGTTTGGTTGCCAGACAAACATGTGCTTCATTCCCC 480

Qy       1114 CCTGGTTAATTTTTACACACCCTAGGAAACATTTCCAAGATCCTGTGATGGCGAGACAAA 1173

Db        481 CCTGGTTAATTTTTACACACCCTAGGAAACATTTCCAAGATCCTGTGATGGCGAGACAAA 540

Qy       1174 TGATCCTTAA-AGAAGGTGTGGGGTCTTTCCCAACCTGAGGATTTCTGAA-AGGTTCACA 1231

Db        541 TGATCCTTAACAGAAGGTGTGGGGTCTTTCCCAACCTGAGGATTTCTGAACAGGTTCACA 600

Qy       1232 GGTTCAATATTTAATGCTTCAGAAGCATGTGAGGTTCCCAACACTGTCAGCAAAAACCTT 1291

Db        601 GGTTCAATATTTAATGCTTCAGAAGCATGTGAGGTTCCCAACACTGTCAGCAAAAACCTT 660

Qy       1292 AGGAGAAAACTTAAAAATATATGAATACATGCGCAATACACAGCTACAGACACACATTCT 1351

Db        661 AGGAGAAAACTTAAAAATATATGAATACATGCGCAATACACAGCTACAGACACACATTCT 720

Qy       1352 GTTGACAA-GGGAAAACCTTCAAAGCATGTTTCTTTCCCTCACCACAACAGAACATGCAG 1410

Db        721 GTTGACAACGGGAAAAGCTTCAAAGCATGTTTCTTTCCCTCACTA-AAAAGAACATGCAG 779

Qy       1411 TACTAAAGCAATATATTTGTGATTCCCCATGTAATTCTTCAATGTTAAACAGTGCAGTCC 1470

Db        780 TACTAAAGCACTATATTTGGTGATTCCCCATGTATTCTTCAATGTTAAACAGTGCAGTCC 839

Qy       1471 TCTTTCGAAAGCTA 1484

Db        840 TCTTTCGAGAGCTA 853
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RESULT 13
BU733808/c
LOCUS       BU733808                 759 bp    mRNA    linear   EST 09-OCT-2002
DEFINITION  UI-E-CK1-aga-d-03-0-UI.s1 UI-E-CK1 Homo sapiens cDNA clone
            UI-E-CK1-aga-d-03-0-UI 3', mRNA sequence.
ACCESSION   BU733808
VERSION     BU733808.1  GI:23661081
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 759)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
   PUBMED   8889548
COMMENT     Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road , 4156  MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
```

Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA sequence: 1-40, >AT_rich#Low_complexity
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES Location/Qualifiers
source 1. .759
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-CK1-aga-d-03-0-UI"
/tissue_type="Retina Foveal and Macular"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-CK1"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-E-CK1 is a normalized cDNA library containing the following tissue(s): Retina Foveal and Macular. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GTCC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI).
TAG_TISSUE=Foveal and Macular Retina
TAG_LIB=UI-E-CK1
TAG_SEQ=GTCC"

ORIGIN

Query Match 44.1%; Score 742.4; DB 13; Length 759;
Best Local Similarity 99.6%; Pred. No. 4.5e-98;
Matches 754; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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Qy        929 GCTTCCGCTTAGAGGTCCTGGCGCCTCGGCACAGCTGCCACGGGCTCTCCTGGGCTTATG 988
              ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        759 GCTTCCGCTTAGAGGTCCTGGCGCCTCGGCACAGCTGCCAC-GGCTCTCCTGGGCTTATG 701

Qy        989 GCCGGTCACAGCCTCAGTGTGACTCCACAGTGGCCCCTGTAGCCGGGCAAGCAGGAGCAG 1048
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        700 GCCGGTCACAGCCTCAGTGTGACTCCACAGTGGCCCCTGTAGCCGGGCAAGCAGGAGCAG 641

Qy       1049 GTCTCTCTGCATCTGTTCTCTGAGGAACTCAAGTTTGGTTGCCAGAAAAAATGTGCTTCAT 1108
              ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db        640 GTCTCTCTGCATCTGTTCTCTGAGGAACTCAAGTNTGGTTGCCAGAAAAAATGTGCTTCAT 581

Qy       1109 TCCCCCCTGGTTAATTTTTACACACCCTAGGAAACATTTCCAAGATCCTGTGATGGCGAG 1168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        580 TCCCCCCTGGTTAATTTTTACACACCCTAGGAAACATTTCCAAGATCCTGTGATGGCGAG 521

Qy       1169 ACAAATGATCCTTAAAGAAGGTGTGGGGTCTTTCCCAACCTGAGGATTTCTGAAAGGTTC 1228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        520 ACAAATGATCCTTAAAGAAGGTGTGGGGTCTTTCCCAACCTGAGGATTTCTGAAAGGTTC 461

Qy       1229 ACAGGTTCAATATTTAATGCTTCAGAAGCATGTGAGGTTCCCAACACTGTCAGCAAAAAC 1288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        460 ACAGGTTCAATATTTAATGCTTCAGAAGCATGTGAGGTTCCCAACACTGTCAGCAAAAAC 401

Qy       1289 CTTAGGAGAAAACTTAAAAATATATGAATACATGCGCAATACACAGCTACAGACACACAT 1348
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Db        400 CTTAGGAGAAAACTTAAAAATATATGAATACATGCGCAATACACAGCTACAGACACACAT 341

Qy       1349 TCTGTTGACAAGGGAAAACCTTCAAAGCATGTTTCTTTCCCTCACCACAACAGAACATGC 1408
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Db        340 TCTGTTGACAAGGGAAAACCTTCAAAGCATGTTTCTTTCCCTCACCACAACAGAACATGC 281

Qy       1409 AGTACTAAAGCAATATATTTGTGATTCCCCATGTAATTCTTCAATGTTAAACAGTGCAGT 1468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        280 AGTACTAAAGCAATATATTTGTGATTCCCCATGTAATTCTTCAATGTTAAACAGTGCAGT 221

Qy       1469 CCTCTTTCGAAAGCTAAGATGACCATGCGCCCTTTCCTCTGTACATATACCCTTAAGAAC 1528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 CCTCTTTCGAAAGCTAAGATGACCATGCGCCCTTTCCTCTGTACATATACCCTTAAGAAC 161

Qy       1529 GCCCCCTCCACACACTGCCCCCCAGTATATGCCGCATTGTACTGCTGTGTTATATGCTAT 1588
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        160 GCCCCCTCCACACACTGCCCCCCAGTATATGCCGCATTGTACTGCTGTGTTATATGCTAT 101

Qy       1589 GTACATGTCAGAAACCATTAGCATTGCATGCAGGTTTCATATTCTTTCTAAGATGGAAAG 1648
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        100 GTACATGTCAGAAACCATTAGCATTGCATGCAGGTTTTATATTCTTTCTAAGATGGAAAG 41

Qy       1649 TAATAAAATATATTTGAAATGTAAAAAAAAAAAAAAA 1685
              ||||||||||||||||||||||||||||||||||||
Db          40 TAATAAAATATATTTGAAATGTAAAAAAAAAAAAAA 4
```

RESULT 14
AK076112
LOCUS AK076112 1665 bp mRNA linear HTC 20-SEP-2003
DEFINITION Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2810410F08 product:small inducible cytokine subfamily B (Cys-X-Cys), member 14, full insert sequence.
ACCESSION AK076112
VERSION AK076112.1 GI:26345085
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5

```
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 1665)
  AUTHORS   Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A.,
            Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y.,
            Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K.,
            Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M.,
            Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K.,
            Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C.,
            Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
            Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y.,
            Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T.,
            Tejima,Y., Toya,T., Yamamura,T., Yamanaka,I., Yasunishi,A.,
            Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.go.jp/
            URL:http://fantom.gsc.riken.go.jp/.
FEATURES             Location/Qualifiers
     source          1. .1665
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                     /mol_type="mRNA"
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                     /db_xref="FANTOM_DB:2810410F08"
                     /db_xref="MGI:1897254"
                     /db_xref="taxon:10090"
                     /clone="2810410F08"
                     /tissue_type="whole body"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="10, 11 days embryo"
     CDS             221. .520
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                     small inducible cytokine subfamily B (Cys-X-Cys), member
                     14 (MGD|MGI:1888514)"
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                     /db_xref="GI:26345086"
                     /translation="MRLLAAALLLLLLALCASRVDGSKCKCSRKGPKIRYSDVKKLEM
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ORIGIN

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  Best Local Similarity   71.5%;  Pred. No. 2.4e-95;
  Matches 1215;  Conservative    0;  Mismatches  357;  Indels  128;  Gaps   15;

Qy         20 GCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGGCGCAGCCGGAGCCAGCAGA 79
Db         39 GCGCGGCACCGCGACAGACGGCAGGAGCACCCATCGACGGGCGTAGCTGGAGCGAGCCGA 98

Qy         80 GCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCTGGGTGGCGTCTCCGGGCCG 139
Db         99 GCAGAGCAGAGAGAGGCGTGCTTGAAACCGAGAACCAAGCCGGGCGGCATCCCCCGGCCG 158

Qy        140 CCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCCACGCCGCGCCCCTCCGGTC 199
Db        159 CCGCACGCACAGGCCGGCGCCCTCCTTGCCTCCCTGCTCCC-CACCGCGCCCCTCCGGCC 217

Qy        200 AGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCTGGCGCTGTACACCGCGCGT 259
Db        218 AGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTCCTGGCGCTGTGCGCCTCGCGC 277

Qy        260 GTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAAGATCCGCTACAGCGACGTG 319
Db        278 GTGGACGGGTCCAAGTGTAAGTGTTCCCGGAAGGGGCCCAAGATCCGCTACAGCGACGTG 337

Qy        320 AAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGAGAAGATGGTTATCATCACC 379
Db        338 AAGAAGCTGGAAATGAAGCCAAAGTACCCACACTGCGAGGAGAAGATGGTTATCGTCACC 397

Qy        380 ACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCTGCACCCCAAGCTGCAGAGC 439
Db        398 ACCAAGAGCATGTCCAGGTACCGGGGCCAGGAGCACTGCCTGCACCCTAAGCTGCAGAGC 457

Qy        440 ACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAAGCGCAGGGTCTACGAAGAA 499
Db        458 ACCAAACGCTTCATCAAGTGGTACAATGCCTGGAACGAGAAGCGCAGGGTCTACGAAGAA 517

Qy        500 TAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTGGGAGACTTGTGCAAAGGAC 559
Db        518 TAGGGTGGACGATCATGGAAAGAAAAACTCCAGGCCAGTTGAGAGACTTCAGCAGAGGAC 577

Qy        560 TTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCCTTT 619
Db        578 TTTGCAGATT----------------------------------AAAATAAAAGCCCTTT 603

Qy        620 CTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGAAGCACTTTTTACCAACGGT 679
Db        604 CTTTCTCACAAGCATAAG--ACAAATTATATATTGCTATGAAGCTCTTCTTACC-AGGGT 660

Qy        680 CAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGATGGGAGACCCATCTCTCTT 739
Db        661 CAGTTTTTACATTTTATAGCTGTGTGTGAAAGGCTTCCAGATGTGAGATCCAGCTCGCCT 720

Qy        740 GTGCTCCAGACTTCATCACAGGCTGCTTTTT------------ATCAAAAAGGGGAAAA 786
Db        721 GCGCACCAGACTTCATTACAAGTGGCTTTTTGCTGGGCGGTTGGCGGGGGGCGGGGGGAC 780

Qy        787 CTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTATACATC 846
Db        781 CTCAAGCCTTTCCTTTTTAAAATAAGGGGTTTTGTATTTGTCCATATGTCACCACACATC 840

Qy        847 TGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTGCAGTGT 906
Db        841 TGAGCTTTATAAGCGCCTGGGAGGAACAGTGAGCATGGTTGAGACCGTTCACAGCACTAC 900

Qy        907 TGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCACAGCTGC 966
Db        901 TGCTCCGCTCCAGGCTTACAAAGCTTCCGCTCAGAGAGCCTGGCGGCTCTGCGCAGCTGC 960

Qy        967 CACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTGGCCCCT 1026
Db        961 CACAGGCTCTCCTGGGCTTATGACTGGTCAGAGTTTCAGTGTGACTCCACTGTGGCCCCT 1020

Qy       1027 GTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAAGTTTGG 1086
Db       1021 GTTGCAGGGCAATTGGGAGCAGGTCCTTCTACATCTGTGCCTAGAGGAACTC-AGTCTAC 1079

Qy       1087 TTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGAAACATT 1146
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Qy       1147 TCCAAGATCCTGTGATGGCGAGACAAATGATCCTTAAAGAAGGTGTGGGGTCTT-TCCCA 1205
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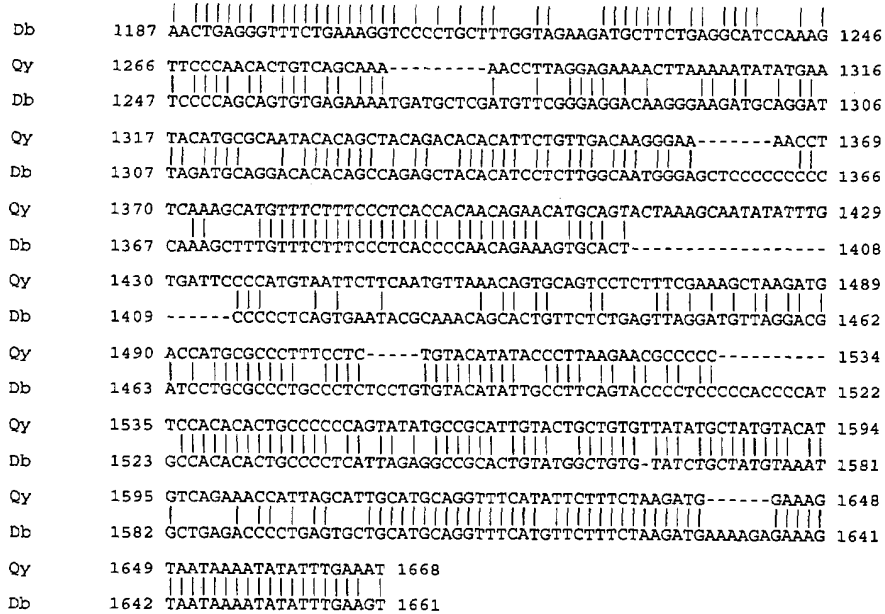

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DEFINITION BX106404 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGp998O22824 ; IMAGE:358893, mRNA sequence.
ACCESSION BX106404
VERSION BX106404.1 GI:27846958
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 722)
AUTHORS Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M., Radelof,U., Schneider,D. and Korn,B.
TITLE Human UnigeneSet - RZPD3
JOURNAL Unpublished (2003)
COMMENT Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGp998O22824.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human UnigeneSet - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer: M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.
FEATURES Location/Qualifiers
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/sex="unknown"
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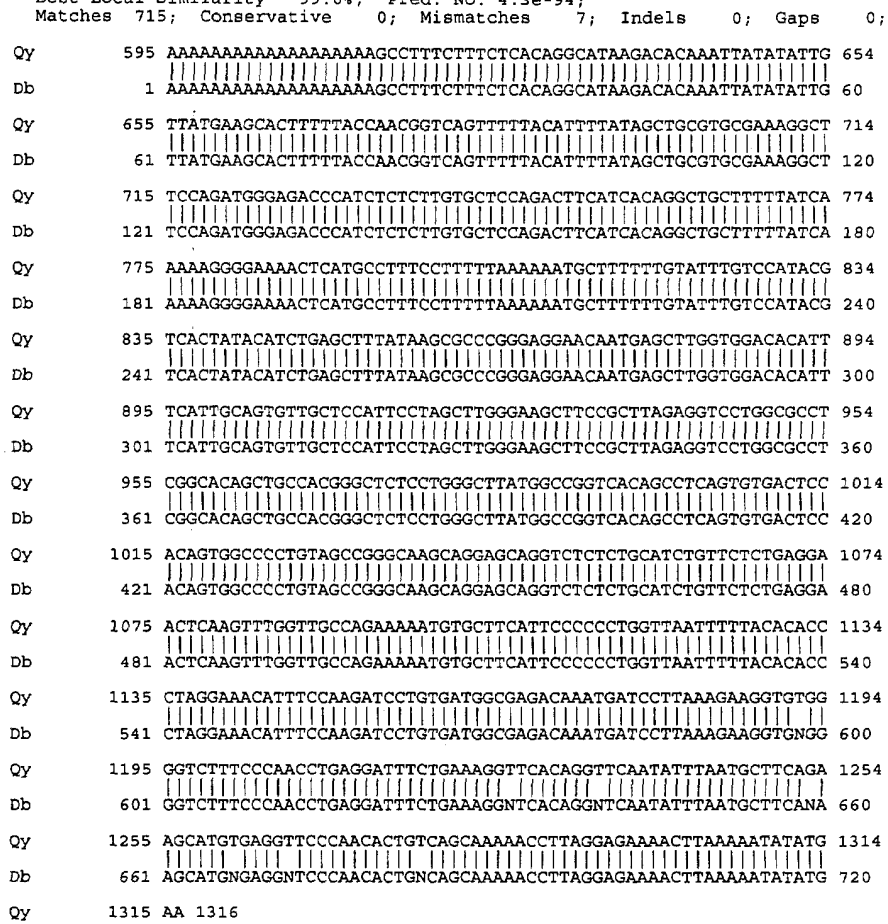
/clone_lib="Soares_fetal_heart_NbHH19W"
/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCATCTTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Patima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NbHL19W."

ORIGIN

Query Match 42.4%; Score 715; DB 13; Length 722;
Best Local Similarity 99.0%; Pred. No. 4.3e-94;
Matches 715; Conservative 0; Mismatches 7; Indels 0; Gaps 0;



Db 721 AA 722

Search completed: April 26, 2004, 08:49:50
Job time : 4605 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 26, 2004, 07:33:10 ; Search time 1852 Seconds
(without alignments)
4102.071 Million cell updates/sec

Title: US-09-978-189-369
Perfect score: 1685
Sequence: 1 gcggagacaagcgcagagcg.....aatgtaaaaaaaaaaaaaaa 1685

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2907579 seqs, 2254313464 residues

Total number of hits satisfying chosen parameters: 5815158

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	1685	100.0	1685	9	US-09-999-832A-369	Sequence 369, App
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ALIGNMENTS

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; Sequence 1, Application US/09816920
; Patent No. US20020119118A1
; GENERAL INFORMATION:
; APPLICANT: Fong,Sherman
; APPLICANT: Goddard,Audrey
; APPLICANT: Hillan,Kenneth J.
; APPLICANT: Roth,Iris
; APPLICANT: Wood,William I.
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING BOLEKINE
; FILE REFERENCE: P1192-2 (US)
; CURRENT APPLICATION NUMBER: US/09/816,920
; CURRENT FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US 60/064,249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: US 60/083,336
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: PCT/US99/05028
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
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; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 7
; SEQ ID NO 1
; LENGTH: 1685
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; ORGANISM: Homo Sapien
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C11
; CURRENT APPLICATION NUMBER: US/09/978,295A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/085697

  Query Match           100.0%;  Score 1685;  DB 9;  Length 1685;
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; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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; CURRENT FILING DATE: 2001-10-16
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; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1685; DB 9; Length 1685;
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Qy        901 CAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCAC 960
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Db        901 CAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCAC 960

Qy        961 AGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTG 1020
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Db        961 AGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTG 1020

Qy       1021 GCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAA 1080
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Db       1021 GCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAA 1080

Qy       1081 GTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGA 1140
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Db       1081 GTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGA 1140

Qy       1141 AACATTTCCAAGATCCTGTGATGGCGAGACAAATGATCCTTAAAGAAGGTGTGGGGTCTT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AACATTTCCAAGATCCTGTGATGGCGAGACAAATGATCCTTAAAGAAGGTGTGGGGTCTT 1200

Qy       1201 TCCCAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATATTTAATGCTTCAGAAGCATG 1260
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Db       1201 TCCCAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATATTTAATGCTTCAGAAGCATG 1260
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Qy       1261 TGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATATGAATACA 1320
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Db       1261 TGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATATGAATACA 1320

Qy       1321 TGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGT 1380
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Db       1321 TGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGT 1380

Qy       1381 TTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATATTTGTGATTCCCCAT 1440
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Db       1381 TTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATATTTGTGATTCCCCAT 1440

Qy       1441 GTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGATGACCATGCGCCC 1500
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Qy       1681 AAAAA 1685
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RESULT 4
US-09-978-192A-369
; Sequence 369, Application US/09978192A
; Patent No. US20020177553A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C9
; CURRENT APPLICATION NUMBER: US/09/978,192A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
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; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1685; DB 9; Length 1685;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1685; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGG 60
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Qy        121 GGGTGGCGTCTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCC 180
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Db        121 GGGTGGCGTCTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCC 180

Qy        181 ACGCCGCGCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCT 240
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Qy        241 GGCGCTGTACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAA 300
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Db        241 GGCGCTGTACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAA 300

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Db        361 GAAGATGGTTATCATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCT 420

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Db        421 GCACCCCAAGCTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAA 480

Qy        481 GCGCAGGGTCTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTG 540
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Db        541 GGAGACTTGTGCAAAGGACTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 600

Qy        601 AAAAAAAAAAAAAGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGA 660
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Db        601 AAAAAAAAAAAAAGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGA 660

Qy        661 AGCACTTTTTACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGA 720
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Db        661 AGCACTTTTTACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGA 720

Qy        721 TGGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGG 780
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Qy        781 GGAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTA 840
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Db        841 TACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTG 900

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Db       1261 TGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATATGAATACA 1320

Qy       1321 TGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGT 1380
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Db       1321 TGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGT 1380

Qy       1381 TTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATATTTGTGATTCCCCAT 1440
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Db       1381 TTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATATTTGTGATTCCCCAT 1440

Qy       1441 GTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGATGACCATGCGCCC 1500
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Db       1441 GTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGATGACCATGCGCCC 1500

Qy       1501 TTTCCTCTGTACATATACCCTTAAGAACGCCCCCTCCACACACTGCCCCCCAGTATATGC 1560
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Qy       1681 AAAAA 1685
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RESULT 5
US-09-999-832A-369
; Sequence 369, Application US/09999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C63
;  CURRENT APPLICATION NUMBER: US/09/999,832A
;  CURRENT FILING DATE:  2001-10-24
;  PRIOR APPLICATION NUMBER: 09/918585
;  PRIOR FILING DATE: 2001-07-30
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
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;  PRIOR FILING DATE: 1997-11-21
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;  PRIOR APPLICATION NUMBER: 60/077632
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;  PRIOR APPLICATION NUMBER: 60/077641
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;  PRIOR APPLICATION NUMBER: 60/078004
;  PRIOR FILING DATE: 1998-03-13
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Query Match 100.0%; Score 1685; DB 9; Length 1685;
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; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
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; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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Query Match 100.0%; Score 1685; DB 10; Length 1685;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1685; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db        541 GGAGACTTGTGCAAAGGACTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 600

Qy        601 AAAAAAAAAAAAAGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAAAAAAAAAAAAGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGA 660

Qy        661 AGCACTTTTTACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGCACTTTTTACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGA 720

Qy        721 TGGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTTATCAAAAAGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTTATCAAAAAGG 780

Qy        781 GGAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GGAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTA 840

Qy        841 TACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTG 900

Qy        901 CAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCAC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCAC 960

Qy        961 AGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTG 1020

Qy       1021 GCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAA 1080

Qy       1081 GTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGA 1140

Qy       1141 AACATTTCCAAGATCCTGTGATGGCGAGACAAATGATCCTTAAAGAAGGTGTGGGGTCTT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AACATTTCCAAGATCCTGTGATGGCGAGACAAATGATCCTTAAAGAAGGTGTGGGGTCTT 1200

Qy       1201 TCCCAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATATTTAATGCTTCAGAAGCATG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TCCCAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATATTTAATGCTTCAGAAGCATG 1260

Qy       1261 TGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATATGAATACA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATATGAATACA 1320

Qy       1321 TGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGT 1380

Qy       1381 TTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATATTTGTGATTCCCCAT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATATTTGTGATTCCCCAT 1440

Qy       1441 GTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGATGACCATGCGCCC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGATGACCATGCGCCC 1500

Qy       1501 TTTCCTCTGTACATATACCCTTAAGAACGCCCCCTCCACACACTGCCCCCCAGTATATGC 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 TTTCCTCTGTACATATACCCTTAAGAACGCCCCCTCCACACACTGCCCCCCAGTATATGC 1560

Qy       1561 CGCATTGTACTGCTGTGTTATATGCTATGTACATGTCAGAAACCATTAGCATTGCATGCA 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CGCATTGTACTGCTGTGTTATATGCTATGTACATGTCAGAAACCATTAGCATTGCATGCA 1620

Qy       1621 GGTTTCATATTCTTTCTAAGATGGAAAGTAATAAAATATATTTGAAATGTAAAAAAAAAA 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GGTTTCATATTCTTTCTAAGATGGAAAGTAATAAAATATATTTGAAATGTAAAAAAAAAA 1680

Qy       1681 AAAAA 1685
              |||||
Db       1681 AAAAA 1685
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RESULT 7
US-09-978-608A-369
; Sequence 369, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey

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;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C22
;  CURRENT APPLICATION NUMBER: US/09/978,608A
;  CURRENT FILING DATE:  2001-10-16
;  NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 369
;    LENGTH: 1685
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-09-978-608A-369

  Query Match           100.0%;  Score 1685;  DB 10;  Length 1685;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1685;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGG 60

Qy         61 CGCAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGCAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCT 120

Qy        121 GGGTGGCGTCTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGTGGCGTCTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCC 180

Qy        181 ACGCCGCGCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACGCCGCGCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCT 240

Qy        241 GGCGCTGTACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGCGCTGTACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAA 300

Qy        301 GATCCGCTACAGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GATCCGCTACAGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGA 360

Qy        361 GAAGATGGTTATCATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAAGATGGTTATCATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCT 420

Qy        421 GCACCCCAAGCTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCACCCCAAGCTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAA 480

Qy        481 GCGCAGGGTCTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCGCAGGGTCTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTG 540

Qy        541 GGAGACTTGTGCAAAGGACTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGAGACTTGTGCAAAGGACTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 600

Qy        601 AAAAAAAAAAAAAGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAAAAAAAAAAAAGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGA 660

Qy        661 AGCACTTTTTACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGCACTTTTTACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGA 720

Qy        721 TGGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGG 780

Qy        781 GGAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GGAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTA 840

Qy        841 TACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTG 900

Qy        901 CAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCAC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCAC 960

Qy        961 AGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTG 1020

Qy       1021 GCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAA 1080

Qy       1081 GTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGA 1140

Qy       1141 AACATTTCCAAGATCCTGTGATGGCGAGACAAATGATCCTTAAAGAAGGTGTGGGGTCTT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AACATTTCCAAGATCCTGTGATGGCGAGACAAATGATCCTTAAAGAAGGTGTGGGGTCTT 1200

Qy       1201 TCCCAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATATTTAATGCTTCAGAAGCATG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TCCCAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATATTTAATGCTTCAGAAGCATG 1260

Qy       1261 TGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATATGAATACA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATATGAATACA 1320

Qy       1321 TGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGT 1380

Qy       1381 TTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATATTTGTGATTCCCCAT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATATTTGTGATTCCCCAT 1440

Qy       1441 GTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGATGACCATGCGCCC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGATGACCATGCGCCC 1500

Qy       1501 TTTCCTCTGTACATATACCCTTAAGAACGCCCCCTCCACACACTGCCCCCCAGTATATGC 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 TTTCCTCTGTACATATACCCTTAAGAACGCCCCCTCCACACACTGCCCCCCAGTATATGC 1560

Qy       1561 CGCATTGTACTGCTGTGTTTATATGCTATGTACATGTCAGAAACCATTAGCATTGCATGCA 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CGCATTGTACTGCTGTGTTTATATGCTATGTACATGTCAGAAACCATTAGCATTGCATGCA 1620

Qy       1621 GGTTTCATATTCTTTCTAAGATGGAAAGTAATAAAATATATTTGAAATGTAAAAAAAAAA 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GGTTTCATATTCTTTCTAAGATGGAAAGTAATAAAATATATTTGAAATGTAAAAAAAAAA 1680

Qy       1681 AAAAA 1685
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Db       1681 AAAAA 1685


RESULT 8
US-09-978-585A-369
; Sequence 369, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C15
;  CURRENT APPLICATION NUMBER: US/09/978,585A
;  CURRENT FILING DATE:  2001-10-16
;  NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 369
;   LENGTH: 1685
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-978-585A-369

  Query Match           100.0%;  Score 1685;  DB 10;  Length 1685;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1685;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGG 60

Qy         61 CGCAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGCAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCT 120

Qy        121 GGGTGGCGTCTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGTGGCGTCTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCC 180

Qy        181 ACGCCGCGCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACGCCGCGCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCT 240

Qy        241 GGCGCTGTACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGCGCTGTACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAA 300

Qy        301 GATCCGCTACAGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GATCCGCTACAGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGA 360

Qy        361 GAAGATGGTTATCATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAAGATGGTTATCATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCT 420

Qy        421 GCACCCCAAGCTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCACCCCAAGCTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAA 480

Qy        481 GCGCAGGGTCTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCGCAGGGTCTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTG 540

Qy        541 GGAGACTTGTGCAAAGGACTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGAGACTTGTGCAAAGGACTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 600

Qy        601 AAAAAAAAAAAAAGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAAAAAAAAAAAAGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGA 660

Qy        661 AGCACTTTTTACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGCACTTTTTACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGA 720

Qy        721 TGGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGG 780

Qy        781 GGAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GGAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTA 840

Qy        841 TACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTG 900

Qy        901 CAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCAC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCAC 960

Qy        961 AGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTG 1020

Qy       1021 GCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAA 1080

Qy       1081 GTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGA 1140

Qy       1141 AACATTTCCAAGATCCTGTGATGGCGAGACAAATGATCCTTAAAGAAGGTGTGGGGTCTT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AACATTTCCAAGATCCTGTGATGGCGAGACAAATGATCCTTAAAGAAGGTGTGGGGTCTT 1200

Qy       1201 TCCCAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATATTTAATGCTTCAGAAGCATG 1260
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Db       1201 TCCCAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATATTTAATGCTTCAGAAGCATG 1260

Qy       1261 TGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATATGAATACA 1320
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Db       1261 TGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATATGAATACA 1320

Qy       1321 TGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGT 1380
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Db       1321 TGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGT 1380

Qy       1381 TTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATATTTGTGATTCCCCAT 1440
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Db       1381 TTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATATTTGTGATTCCCCAT 1440

Qy       1441 GTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGATGACCATGCGCCC 1500
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Db       1441 GTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGATGACCATGCGCCC 1500

Qy       1501 TTTCCTCTGTACATATACCCTTAAGAACGCCCCCTCCACACACTGCCCCCCAGTATATGC 1560
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Db       1561 CGCATTGTACTGCTGTGTTATATGCTATGTACATGTCAGAAACCATTAGCATTGCATGCA 1620

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Qy       1681 AAAAA 1685
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Db       1681 AAAAA 1685
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RESULT 9
US-09-978-191A-369
; Sequence 369, Application US/09978191A
; Publication No. US20030050239A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C4
; CURRENT APPLICATION NUMBER: US/09/978,191A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1685; DB 10; Length 1685;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1685; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 CGCAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCT 120
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Db         61 CGCAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCT 120

Qy        121 GGGTGGCGTCTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCC 180
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Qy        181 ACGCCGCGCCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCT 240
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Db        181 ACGCCGCGCCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCT 240

Qy        241 GGCGCTGTACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAA 300
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Db        241 GGCGCTGTACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAA 300

Qy        301 GATCCGCTACAGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGA 360
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Qy        361 GAAGATGGTTATCATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCT 420
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Db        361 GAAGATGGTTATCATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCT 420

Qy        421 GCACCCCAAGCTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAA 480
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Db        541 GGAGACTTGTGCAAAGGACTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 600

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Db        661 AGCACTTTTTACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGA 720

Qy        721 TGGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGG 780

Qy        781 GGAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTA 840
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Db        841 TACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTG 900

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Db       1321 TGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGT 1380

Qy       1381 TTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATATTTGTGATTCCCCAT 1440
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Db       1381 TTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATATTTGTGATTCCCCAT 1440

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Qy       1681 AAAAA 1685
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RESULT 10
US-09-978-403A-369
; Sequence 369, Application US/09978403A
; Publication No. US20030050240A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C17
;  CURRENT APPLICATION NUMBER: US/09/978,403A
;  CURRENT FILING DATE:  2002-03-19
;  PRIOR APPLICATION NUMBER: 09/918585
;  PRIOR FILING DATE: 2001-07-30
;  PRIOR APPLICATION NUMBER: 60/062250
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Query Match 100.0%; Score 1685; DB 10; Length 1685;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1685; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGG 60

Qy         61 CGCAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCT 120
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Qy        121 GGGTGGCGTCTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCC 180
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Db        661 AGCACTTTTTACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGA 720
Qy        721 TGGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGG 780
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Qy        781 GGAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTA 840
Db        781 GGAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTA 840
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Qy        901 CAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCAC 960
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Qy        961 AGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTG 1020
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; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1685; DB 10; Length 1685;
Best Local Similarity 100.0%; Pred. No. 0;

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Db          1 GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGG 60

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGCAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCT 120

Qy        121 GGGTGGCGTCTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCC 180
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Db        121 GGGTGGCGTCTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCC 180

Qy        181 ACGCCGCGCCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCT 240
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Db        181 ACGCCGCGCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCT 240

Qy        241 GGCGCTGTACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAA 300
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Qy        301 GATCCGCTACAGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGA 360
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Db        361 GAAGATGGTTATCATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCT 420

Qy        421 GCACCCCAAGCTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAA 480
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Qy        481 GCGCAGGGTCTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTG 540
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Qy        541 GGAGACTTGTGCAAAGGACTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        601 AAAAAAAAAAAAAGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGA 660
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Qy        721 TGGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGG 780
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Qy        781 GGAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTA 840
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Db        781 GGAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTA 840

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Db        841 TACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTG 900

Qy        901 CAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCAC 960
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Db        901 CAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCAC 960

Qy        961 AGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTG 1020
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Db        961 AGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTG 1020

Qy       1021 GCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAA 1080
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Db       1021 GCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAA 1080

Qy       1081 GTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGA 1140
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Db       1081 GTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGA 1140

Qy       1141 AACATTTCCAAGATCCTGTGATGGCGAGACAAATGATCCTTAAAGAAGGTGTGGGGTCTT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AACATTTCCAAGATCCTGTGATGGCGAGACAAATGATCCTTAAAGAAGGTGTGGGGTCTT 1200

Qy       1201 TCCCAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATATTTAATGCTTCAGAAGCATG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TCCCAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATATTTAATGCTTCAGAAGCATG 1260

Qy       1261 TGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATATGAATACA 1320
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Db       1261 TGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATATGAATACA 1320

Qy       1321 TGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGT 1380
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Db       1321 TGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGT 1380

Qy       1381 TTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATATTTGTGATTCCCCAT 1440
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Db       1381 TTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATATTTGTGATTCCCCAT 1440

Qy       1441 GTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGATGACCATGCGCCC 1500
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Db       1441 GTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGATGACCATGCGCCC 1500

Qy       1501 TTTCCTCTGTACATATACCCTTAAGAACGCCCCCTCCACACACTGCCCCCCAGTATATGC 1560
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Db       1501 TTTCCTCTGTACATATACCCTTAAGAACGCCCCCTCCACACACTGCCCCCCAGTATATGC 1560

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Db       1561 CGCATTGTACTGCTGTGTTTATATGCTATGTACATGTCAGAAACCATTAGCATTGCATGCA 1620

Qy       1621 GGTTTCATATTCTTTCTAAGATGGAAAGTAATAAAATATATTTGAAATGTAAAAAAAAAA 1680
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Db       1621 GGTTTCATATTCTTTCTAAGATGGAAAGTAATAAAATATATTTGAAATGTAAAAAAAAAA 1680

Qy       1681 AAAAA 1685
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Db       1681 AAAAA 1685
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RESULT 12
US-09-999-833A-369
; Sequence 369, Application US/09999833A
; Publication No. US20030054405A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C65
; CURRENT APPLICATION NUMBER: US/09/999,833A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
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; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1685; DB 10; Length 1685;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1685; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGG 60
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Db          1 GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGG 60

Qy         61 CGCAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCT 120
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Db         61 CGCAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCT 120

Qy        121 GGGTGGCGTCTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCC 180
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Db        121 GGGTGGCGTCTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCC 180

Qy        181 ACGCCGCGCCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCT 240
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Db        181 ACGCCGCGCCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCT 240

Qy        241 GGCGCTGTACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGCGCTGTACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAA 300

Qy        301 GATCCGCTACAGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGA 360
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Db        301 GATCCGCTACAGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGA 360

Qy        361 GAAGATGGTTATCATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCT 420
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Db        361 GAAGATGGTTATCATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCT 420

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Db        421 GCACCCCAAGCTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAA 480

Qy        481 GCGCAGGGTCTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTG 540
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Db        481 GCGCAGGGTCTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTG 540

Qy        541 GGAGACTTGTGCAAAGGACTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGAGACTTGTGCAAAGGACTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 600

Qy        601 AAAAAAAAAAAAAAGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGA 660
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Db        601 AAAAAAAAAAAAAAGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGA 660

Qy        661 AGCACTTTTTACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGCACTTTTTACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGA 720

Qy        721 TGGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTTATCAAAAAGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTTATCAAAAAGG 780

Qy        781 GGAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTA 840
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Db        781 GGAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTA 840

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Qy       1021 GCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAA 1080
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Db       1201 TCCCAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATATTTAATGCTTCAGAAGCATG 1260

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Db       1261 TGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATATGAATACA 1320

Qy       1321 TGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGT 1380
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Db       1321 TGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGT 1380

Qy       1381 TTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATATTTTGTGATTCCCCAT 1440
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Db       1381 TTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATATTTTGTGATTCCCCAT 1440

Qy       1441 GTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGATGACCATGCGCCC 1500
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Qy       1681 AAAAA 1685
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RESULT 13
US-09-981-915A-369
; Sequence 369, Application US/09981915A
; Publication No. US20030054986A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C12
;  CURRENT APPLICATION NUMBER: US/09/981,915A
;  CURRENT FILING DATE:  2001-10-16
;  PRIOR APPLICATION NUMBER: 09/918585
;  PRIOR FILING DATE: 2001-07-30
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/064249
;  PRIOR FILING DATE: 1997-11-03
;  PRIOR APPLICATION NUMBER: 60/065311
;  PRIOR FILING DATE: 1997-11-13
;  PRIOR APPLICATION NUMBER: 60/066364
;  PRIOR FILING DATE: 1997-11-21
;  PRIOR APPLICATION NUMBER: 60/077450
;  PRIOR FILING DATE: 1998-03-10
;  PRIOR APPLICATION NUMBER: 60/077632
;  PRIOR FILING DATE: 1998-03-11
;  PRIOR APPLICATION NUMBER: 60/077641
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; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1685; DB 10; Length 1685;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1685; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        241 GGCGCTGTACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAA 300
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Db       1201 TCCCAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATATTTAATGCTTCAGAAGCATG 1260

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RESULT 14
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; Publication No. US20030055216A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C14
; CURRENT APPLICATION NUMBER: US/09/978,824
; CURRENT FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1685; DB 10; Length 1685;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1685; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGG 60
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Db          1 GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGG 60

Qy         61 CGCAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCT 120
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Db         61 CGCAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCT 120

Qy        121 GGGTGGCGTCTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCC 180
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Db        121 GGGTGGCGTCTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCC 180

Qy        181 ACGCCGCGCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCT 240
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Db        181 ACGCCGCGCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCT 240

Qy        241 GGCGCTGTACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAA 300
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Db        241 GGCGCTGTACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAA 300

Qy        301 GATCCGCTACAGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGA 360
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Db        301 GATCCGCTACAGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGA 360

Qy        361 GAAGATGGTTATCATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCT 420
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Db        361 GAAGATGGTTATCATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCT 420

Qy        421 GCACCCCAAGCTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAA 480
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Qy        481 GCGCAGGGTCTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTG 540
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Qy        541 GGAGACTTGTGCAAAGGACTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 600
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Db        541 GGAGACTTGTGCAAAGGACTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 600

Qy        601 AAAAAAAAAAAAAGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGA 660
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Qy       721 TGGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGG 780
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Qy       781 GGAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTA 840
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Db       781 GGAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTA 840

Qy       841 TACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTG 900
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Qy       901 CAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCAC 960
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Qy      1081 GTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGA 1140
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Qy      1201 TCCCAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATATTTAATGCTTCAGAAGCATG 1260
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Qy      1681 AAAAA 1685
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RESULT 15
US-09-918-585A-369
; Sequence 369, Application US/09918585A
; Publication No. US20030060406A1

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; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C1
;  CURRENT APPLICATION NUMBER: US/09/918,585A
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086023

Query Match 100.0%; Score 1685; DB 10; Length 1685;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1685; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1681 AAAAA 1685
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 26, 2004, 03:31:29 ; Search time 6718 Seconds
(without alignments)
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Title: US-09-978-189-369
Perfect score: 1685
Sequence: 1 gcggagacaagcgcagagcg.....aatgtaaaaaaaaaaaaaaa 1685

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

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Minimum DB seq length: 0
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
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2		1685	100.0	1685	9	AY358906	AY358906 Homo sapi
3		1640.4	97.4	1677	6	AX136401	AX136401 Sequence
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5		1640.4	97.4	1677	9	AK075514	AK075514 Homo sapi
6		1449.2	86.0	1865	6	AR379680	AR379680 Sequence
7		1433.2	85.1	1503	9	AF144103	AF144103 Homo sapi
8	c	1179.2	70.0	108123	9	AC034206	AC034206 Homo sapi
9	c	1177.2	69.9	134506	9	AC005738	AC005738 Homo sapi
10	c	1175.6	69.8	79970	2	AC011428	AC011428 Homo sapi
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17		976.2	57.9	1962	6	AX011681	AX011681 Sequence
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ALIGNMENTS

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LOCUS AX565505 1685 bp DNA linear PAT 29-NOV-2002
DEFINITION Sequence 1 from Patent WO02077028.
ACCESSION AX565505
VERSION AX565505.1 GI:26000857
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Fong,S., Goddard,A., Hillan,K.J., Roth,I. and Wood,W.I.
TITLE Polypeptides and nucleic acids for bolekine
JOURNAL Patent: WO 02077028-A 1 03-OCT-2002;

Genentech, Inc. (US)

FEATURES Location/Qualifiers
source 1. .1685
/organism="Homo sapiens"
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ORIGIN

Query Match 100.0%; Score 1685; DB 6; Length 1685;
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Matches 1685; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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DEFINITION Homo sapiens clone DNA39523 SCYB14 (UNQ240) mRNA, complete cds.
ACCESSION AY358906
VERSION AY358906.1 GI:37182929
KEYWORDS FLI_CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1685)
AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,

Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V., Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K., Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z., Goddard,A., Wood,W.I. and Godowski,P.
TITLE The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment
JOURNAL Genome Res. 13 (10), 2265-2270 (2003)
PUBMED 12975309
REFERENCE 2 (bases 1 to 1685)
AUTHORS Clark,H.F.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA

FEATURES Location/Qualifiers

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1685; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
AX136401
LOCUS AX136401 1677 bp DNA linear PAT 30-MAY-2001
DEFINITION Sequence 323 from Patent EP1067182.
ACCESSION AX136401
VERSION AX136401.1 GI:14272805
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.
TITLE Secretory protein or membrane protein
JOURNAL Patent: EP 1067182-A 323 10-JAN-2001;
Helix Research Institute (JP)

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ORIGIN

Query Match 97.4%; Score 1640.4; DB 6; Length 1677;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1660; Conservative 0; Mismatches 1; Indels 9; Gaps 1;

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Qy          1 GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGG 60
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Db         17 GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGG 76

Qy         61 CGCAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCT 120
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Db         77 CGCAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCT 136

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RESULT 4
BD123653
LOCUS       BD123653                1677 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Secretory protein or membrane protein.
ACCESSION   BD123653
VERSION     BD123653.1  GI:23218598
KEYWORDS    JP 2002017376-A/162.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1677)
  AUTHORS   Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and
            Hayashi,K.
  TITLE     Secretory protein or membrane protein
  JOURNAL   Patent: JP 2002017376-A 162 22-JAN-2002;
            HELIX RESEARCH INSTITUTE
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002017376-A/162
            PD   22-JAN-2002
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            PI   TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,YURI KAWAI,TOMOYASU
            PI   SUGIYAMA,
            PI   KOJI HAYASHI
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ORIGIN

  Query Match           97.4%;  Score 1640.4;  DB 6;  Length 1677;
  Best Local Similarity   99.4%;  Pred. No. 0;
  Matches 1660;  Conservative    0;  Mismatches    1;  Indels    9;  Gaps    1;

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Qy        181 ACGCCGCGCCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCT 240
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Qy        661 AGCACTTTTTACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGA 720
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Qy        721 TGGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGG 780
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Db        908 CAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCAC 967

Qy        961 AGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTG 1020
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Db        968 AGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTG 1027

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Qy       1381 TTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATATTTGTGATTCCCCAT 1440
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Qy       1621 GGTTTCATATTCTTTCTAAGATGGAAAGTAATAAAATATATTTGAAATGT 1670
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AK075514
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DEFINITION  Homo sapiens cDNA PSEC0212 fis, clone HEMBA1003764, highly similar
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ACCESSION   AK075514
VERSION     AK075514.1  GI:22761706
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ota,T., Nishikawa,T., Suzuki,Y., Kawai-Hio,Y., Hayashi,K.,
            Ishii,S., Saito,K., Yamamoto,J., Wakamatsu,A., Nagai,T.,
            Nakamura,Y., Nagahari,K., Sugano,S. and Isogai,T.
  TITLE     HRI human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1677)
  AUTHORS   Isogai,T. and Yamamoto,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-MAR-2002) Takao Isogai, Helix Research Institute,
            Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT     HRI human cDNA sequencing project; cDNA 5'- & 3'-end one pass
            sequencing, clone selection and full insert sequencing: Helix
            Research Institute (supported by Japan Key Technology Center etc.);
            cDNA library construction: Institute of Medical Science, University
            of Tokyo, Laboratory of Genome Structure, Human Genome Center.
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ORIGIN

  Query Match             97.4%;  Score 1640.4;  DB 9;  Length 1677;
  Best Local Similarity   99.4%;  Pred. No. 0;
  Matches 1660;  Conservative    0;  Mismatches    1;  Indels    9;  Gaps    1;

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Db         17 GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGG 76

Qy         61 CGCAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCT 120
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Db         77 CGCAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCT 136

Qy        121 GGGTGGCGTCTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCC 180
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Qy        181 ACGCCGCGCCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCT 240
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Qy        361 GAAGATGGTTATCATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCT 420
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Db        437 GCACCCCAAGCTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAA 496

Qy        481 GCGCAGGGTCTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        497 GCGCAGGGTCTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTG 556

Qy        541 GGAGACTTGTGCAAAGGACTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 600
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        557 GGAGACTTGTGCAAAGGACTTTGCAGATT---------AAAAAAAAAAAAAAAAAAAAAA 607

Qy        601 AAAAAAAAAAAAAGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGA 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        608 AAAAAAAAAAAAAGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGA 667

Qy        661 AGCACTTTTTACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGA 720
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        668 AGCACTTTTTACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGA 727

Qy        721 TGGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTTATCAAAAAGG 780
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        728 TGGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTTATCAAAAAGG 787

Qy        781 GGAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTA 840
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        788 GGAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTA 847

Qy        841 TACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTG 900
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        848 TACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTG 907

Qy        901 CAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCAC 960
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        908 CAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCAC 967

Qy        961 AGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTG 1020
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        968 AGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTG 1027

Qy       1021 GCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAA 1080
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1028 GCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAA 1087

Qy       1081 GTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGA 1140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1088 GTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGA 1147

Qy       1141 AACATTTCCAAGATCCTGTGATGGCGAGACAAATGATCCTTAAAGAAGGTGTGGGGTCTT 1200
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1148 AACATTTCCAAGATCCTGTGATGGCGAGACAAATGATCCTTAAAGAAGGTGTGGGGTCTT 1207
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Qy       1201 TCCCAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATATTTAATGCTTCAGAAGCATG 1260
Db       1208 TCCCATCCTGAGGATTTCTGAAAGGTTCACAGGTTCAATATTTAATGCTTCAGAAGCATG 1267

Qy       1261 TGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATATGAATACA 1320
Db       1268 TGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATATGAATACA 1327

Qy       1321 TGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGT 1380
Db       1328 TGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGT 1387

Qy       1381 TTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATATTTGTGATTCCCCAT 1440
Db       1388 TTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATATTTGTGATTCCCCAT 1447

Qy       1441 GTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGATGACCATGCGCCC 1500
Db       1448 GTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGATGACCATGCGCCC 1507

Qy       1501 TTTCCTCTGTACATATACCCTTAAGAACGCCCCCTCCACACACTGCCCCCCAGTATATGC 1560
Db       1508 TTTCCTCTGTACATATACCCTTAAGAACGCCCCCTCCACACACTGCCCCCCAGTATATGC 1567

Qy       1561 CGCATTGTACTGCTGTGTTATATGCTATGTACATGTCAGAAACCATTAGCATTGCATGCA 1620
Db       1568 CGCATTGTACTGCTGTGTTATATGCTATGTACATGTCAGAAACCATTAGCATTGCATGCA 1627

Qy       1621 GGTTTCATATTCTTTCTAAGATGGAAAGTAATAAAATATATTTGAAATGT 1670
Db       1628 GGTTTCATATTCTTTCTAAGATGGAAAGTAATAAAATATATTTGAAATGT 1677
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RESULT 6
AR379680
LOCUS AR379680 1865 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 225 from patent US 6607879.
ACCESSION AR379680
VERSION AR379680.1 GI:40087314
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1865)
AUTHORS Cocks,B.G., Stuart,S.G. and Seilhamer,J.J.
TITLE Compositions for the detection of blood cell and immunological response gene expression
JOURNAL Patent: US 6607879-A 225 19-AUG-2003;
FEATURES Location/Qualifiers
source 1. .1865
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 86.0%; Score 1449.2; DB 6; Length 1865;
Best Local Similarity 94.6%; Pred. No. 3.1e-287;
Matches 1604; Conservative 0; Mismatches 57; Indels 34; Gaps 11;

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Qy          1 GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGG 60
Db        172 GCGGAGACAAGCGCAGAGCGCAGCCNACGGCCACAGACAGCCCTGGGCATCCACCGACGG 231

Qy         61 CGCAGCCGGAGCCAGCAGAGCCGGAAGGCGC-GCCCCGGGCAGAGAAAGCCGAGCAGAGC 119
Db        232 CGCA-CNGNGGCCAGCAGAGCCGGAAGGCGCGGCCCCGGGCAGAGAAAGCCGAGCAGAGC 290

Qy        120 TGGGTGGCGTCTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCC 179
Db        291 TGGGTGGCGTCTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCC 350

Qy        180 CACGCCGCGCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGC 239
Db        351 CACGCCGCGCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCNNNNNNNNNNNNNNNNN 410

Qy        240 TGGCGCTGTACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCA 299
Db        411 NNNNNNNNTACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCA 470

Qy        300 AGATCCGCTACAGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGG 359
Db        471 AGATCCGCTACAGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGG 530

Qy        360 AGAAGATGGTTATCATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCC 419
Db        531 AGAAGATGGTTATCATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCC 590

Qy        420 TGCACCCCAAGCTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGA 479
Db        591 TGCACCCCAAGCTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGA 650

Qy        480 AGCGCAGGGTCTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTT 539
Db        651 AGCGCAGGGTCTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTT 710

Qy        540 GGGAGACTTGTGCAAAGGACTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 599
Db        711 GGGAGACTTGTGCAAAGGACTTTGCAGATT----------AAANNNNAA 749

Qy        600 AAAAAAAAAAAAAAGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATG 659
Db        750 NATNAAANNAANNNGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATG 809

Qy        660 AAGCACTTTTTA-CCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCA 718
Db        810 AAGCACTTTTTACCCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCA 869

Qy        719 GATGGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTATCAAAAA 778
Db        870 GATGGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTATCAAAAA 929

Qy        779 GGGGAAAACTCATGCCTTTCCTTTTT-AAAAAATGCTTTTTTGTATTTGTCCATACGTCA 837
Db        930 GGGGAAAACTCATGCCTTTCCTTTTTAAAAAAATGCTTTTTTGTATTTGTCCATACGTCA 989

Qy        838 CTATACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCA 897
Db        990 CTATACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCA 1049

Qy        898 TTGCAGTGTTGCTCCATTCCTAGCTTGGGAAGC-TTCCGCTTAGAGGTCCTGGCGCCTCG 956
Db       1050 TTGCAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTTCCGCTTAGAGGTCCTGGCGCCTCG 1109

Qy        957 GCACAGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCAC 1016
Db       1110 GCACAGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCAC 1169

Qy       1017 AGTGGCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAAC 1076
Db       1170 AGTGGCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAAC 1229

Qy       1077 TCAAGTTTGGTTGCCAGAAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCT 1136
Db       1230 TCAAGTTTGGTTGCCAGAAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACGGCCT 1289

Qy       1137 --AGGAAACATTTCCAA-GATCCTGTGATGGCGAGACAAATGATCCTTAAA-GAAGGTGT 1192
Db       1290 TAGGGAAACATTTCCAAGGATCCTGTGATGGCGAGACAAATGATCCTTAAAGGAAGGTGT 1349

Qy       1193 GGGGTCTTT--CCCAACCTGAGGATTTCTGAAAGGTT--CACAGGTTCAATATTTAATGC 1248
Db       1350 GGGGTCTTTTCCCAACCTGAGGGATTTCTGAAAGGTTTCACAGGTTTCAATATTTAATGC 1409

Qy       1249 TTCAGAAGCATGTGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAA 1308
Db       1410 TTCAGAAGCATGTGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAA 1469
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Qy       1309 TATATGAATACATGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACC 1368
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1470 TATATGAATACATGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACC 1529

Qy       1369 TTCAAAGCATGTTTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATATTT 1428
             |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       1530 TTCAAAGCATGTTTCTTTCCCTCACCACAACAGGACATGCAGTACTAAAGCAATATATTT 1589

Qy       1429 GTGATTCCCCATGTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGAT 1488
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1590 GTGATTCCCCATGTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGAT 1649

Qy       1489 GACCATGCGCCCTTTCCTCTGTACATATACCCTTAAGAACGCCCCCTCCACACACTGCCC 1548
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 GACCATGCGCCCTTTCCTCTGTACATATACCCTTAAGAACGCCCCCTCCACACACTGCCC 1709

Qy       1549 CCCAGTATATGCCGCATTGTACTGCTGTGTTATATGCTATGTACATGTCAGAAACCATTA 1608
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1710 CCCAGTATATGCCGCATTGTACTGCTGTGTTATATGCTATGTACATGTCAGAAACCATTA 1769

Qy       1609 GCATTGCATGCAGGTTTCATATTCTTTCTAAGATGGAAAGTAATAAAATATATTTGAAAT 1668
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1770 GCATTGCATGCAGGTTTCATATTCTTTCTAAGATGGAAAGTAATAAAATATATTTGAAAT 1829

Qy       1669 GTAAAAAAAAAAAAA 1683
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Db       1830 GTAAAAAAAAAAAAA 1844
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RESULT 7
AF144103
LOCUS       AF144103               1503 bp    mRNA    linear   PRI 15-JUN-1999
DEFINITION  Homo sapiens NJAC protein (NJAC) mRNA, complete cds.
ACCESSION   AF144103
VERSION     AF144103.1  GI:5059165
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1503)
  AUTHORS   Same.
  TITLE     Identification of a novel chemokine family member with altered
            expression in human head and neck squamous cell carcinoma
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1503)
  AUTHORS   Frederick,M.F., Henderson,Y., Xu,X., El-Naggar,A.K., Wu,H.,
            Hudson,J.M. and Clayman,G.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-APR-1999) Head and Neck Surgery, M.D. Anderson Cancer
            Cr, 1515 Holcombe Box 69, Houston, TX 77005, USA
FEATURES             Location/Qualifiers
     source          1. .1503
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="5"
                     /map="5q23-q31"
                     /tissue_type="normal oral epithelial"
     gene            1. .1503
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     CDS             8. .307
                     /gene="NJAC"
                     /note="CXC chemokine; putative CXC chemokine similar to
                     BRAK"
                     /codon_start=1
                     /product="NJAC protein"
                     /protein_id="AAD38944.1"
                     /db_xref="GI:5059166"
                     /translation="MRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEM
                     KPKYPHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE"
ORIGIN
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Query Match           85.1%;  Score 1433.2;  DB 9;  Length 1503;
Best Local Similarity 98.5%;  Pred. No. 5.7e-284;
Matches 1465;  Conservative    0;  Mismatches    3;  Indels   20;  Gaps    1;

Qy        196 GGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCTGGCGCTGTACACCGC 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCTGGCGCTGTACACCGC 60

Qy        256 GCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAAGATCCGCTACAGCGA 315
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAAGATCCGCTACAGCGA 120

Qy        316 CGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGAGAAGATGGTTATCAT 375
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGAGAAGATGGTTATCAT 180

Qy        376 CACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCTGCACCCCAAGCTGCA 435
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCTGCACCCCAAGCTGCA 240

Qy        436 GAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAAGCGCAGGGTCTACGA 495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAAGCGCAGGGTCTACGA 300

Qy        496 AGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTGGGAGACTTGTGCAAA 555
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTGGGAGACTTGTGCAAA 360

Qy        556 GGACTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGC 615
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGACTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAA----------C 400

Qy        616 CTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGAAGCACTTTTTACCAA 675
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        401 CTTTCTTTCTCACAGGCATAAGACACAAATTCTATATTGTTATGAAGCACTTTTTACCAA 460

Qy        676 CGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGATGGGAGACCCATCTC 735
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Db        461 CGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGATGGGAGACCCATCTC 520

Qy        736 TCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGGGGAAAACTCATGCCT 795
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        521 TCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGGGGAAAACTCATGCCT 580

Qy        796 TTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTATACATCTGAGCTTTA 855
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        581 TTCCTTTTTAAAAAATGCTTTTTTGCATTTGTCCATACGTCGCTATACATCTGAGCTTTA 640

Qy        856 TAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTGCAGTGTTGCTCCATT 915
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        641 TAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTGCAGTGTTGCTCCATT 700

Qy        916 CCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCACAGCTGCCACGGGCTC 975
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        701 CCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCACAGCTGCCACGGGCTC 760

Qy        976 TCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTGGCCCCTGTAGCCGGG 1035
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Db        761 TCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTGGCCCCTGTAGCCGGG 820

Qy       1036 CAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAAGTTTGGTTGCCAGAA 1095
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        821 CAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAAGTTTGGTTGCCAGAA 880

Qy       1096 AAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGAAACATTTCCAAGATC 1155
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        881 AAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGAAACATTTCCAAGATC 940

Qy       1156 CTGTGATGGCGAGACAAATGATCCTTAAAGAAGGTGTGGGGTCTTTCCCAACCTGAGGAT 1215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        941 CTGTGATGGCGAGACAAATGATCCTTAAAGAAGGTGTGGGGTCTTTCCCAACCTGAGGAT 1000
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Qy       1216 TTCTGAAAGGTTCACAGGTTCAATATTTAATGCTTCAGAAGCATGTGAGGTTCCCAACAC 1275
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Db       1001 TTCTGAAAGGTTCACAGGTTCAATATTTAATGCTTCAGAAGCATGTGAGGTTCCCAACAC 1060

Qy       1276 TGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATATGAATACATGCGCAATACACAGC 1335
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1061 TGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATATGAATACATGCGCAATACACAGC 1120

Qy       1336 TACAGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGTTTCTTTCCCTCACCA 1395
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1121 TACAGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGTTTCTTTCCCTCACCA 1180

Qy       1396 CAACAGAACATGCAGTACTAAAGCAATATATTTGTGATTCCCCATGTAATTCTTCAATGT 1455
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1181 CAACAGAACATGCAGTACTAAAGCAATATATTTGTGATTCCCCATGTAATTCTTCAATGT 1240

Qy       1456 TAAACAGTGCAGTCCTCTTTCGAAAGCTAAGATGACCATGCGCCCTTTCCTCTGTACATA 1515
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1241 TAAACAGTGCAGTCCTCTTTCGAAAGCTAAGATGACCATGCGCCCTTTCCTCTGTACATA 1300

Qy       1516 TACCCTTAAGAACGCCCCCTCCACACACTGCCCCCCCAGTATATGCCGCATTGTACTGCTG 1575
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1301 TACCCTTAAGAACGCCCCCTCCACACACTGCCCCCCCAGTATATGCCGCATTGTACTGCTG 1360

Qy       1576 TGTTATATGCTATGTACATGTCAGAAACCATTAGCATTGCATGCAGGTTTCATATTCTTT 1635
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1361 TGTTATATGCTATGTACATGTCAGAAACCATTAGCATTGCATGCAGGTTTCATATTCTTT 1420

Qy       1636 CTAAGATGGAAAGTAATAAAATATATTTGAAATGTAAAAAAAAAAAAA 1683
             ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1421 CTAAGATGGAAAGTAATAAAATATATTTGAAATGTAAAAAAAAAAAAA 1468
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RESULT 8
AC034206/c

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LOCUS       AC034206               108123 bp    DNA     linear   PRI 20-JUL-2001
DEFINITION  Homo sapiens chromosome 5 clone CTC-321K16, complete sequence.
ACCESSION   AC034206
VERSION     AC034206.4  GI:14518406
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 108123)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 108123)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-APR-2000) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE   3  (bases 1 to 108123)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell
            Drive, Walnut Creek, CA 94598, USA
REFERENCE   4  (bases 1 to 108123)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2001) DOE Joint Genome Institute, 2800 Mitchell
            Drive, Walnut Creek, CA 94598, USA
COMMENT     On Jun 21, 2001 this sequence version replaced gi:9256720.
            Draft Sequence Produced by DOE Joint Genome Institute
            www.jgi.doe.gov
            Finishing Completed at Stanford Human Genome Center
            www-shgc.stanford.edu
            Quality: Phrap Quality >=40 99.5% of Sequence;
            Estimated Total Number of Errors is 0.2.
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Query Match 70.0%; Score 1179.2; DB 9; Length 108123;
Best Local Similarity 99.7%; Pred. No. 1.8e-231;
Matches 1192; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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Db      17579 CCCAGGGTCTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTGG 17520

Qy        542 GAGACTTGTGCAAAGGACTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 601
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Db      17519 GAGACTTGTGCAAAGGACTTTGCAGATT-AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 17461

Qy        602 AAAAAAAAAAAAAGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGAA 661
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Db      17460 AAAAAAAAAAAAAGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGAA 17401

Qy        662 GCACTTTTTACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGAT 721
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Db      17400 GCACTTTTTACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGAT 17341

Qy        722 GGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGGG 781
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Qy       1142 ACATTTCCAAGATCCTGTGATGGCGAGACAAATGATCCTTAAAGAAGGTGTGGGGTCTTT 1201
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Qy       1322 GCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGTT 1381
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RESULT 9
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DEFINITION  Homo sapiens chromosome 5, BAC clone 7g12 (LBNL H126), complete
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ACCESSION   AC005738 AC004619 L81405 L81406 L81678 L81679 L81680 L81860 L81861
            L81862 AC001042 AC001043 AC001520
VERSION     AC005738.1  GI:3687213
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 134506)
  AUTHORS   Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M.,
            Kadner,K., Miguel,T., Miller,C., Pitluck,S., Pollard,M.,
            Rojeski,H., Subramanian,S. and Martin,C.H.
  TITLE     Sequencing of human chromosome 5
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 134506)
  AUTHORS   Ricke,D.O.
  TITLE     Large Scale Sequence Analysis and Annotation with the Sequence
            Comparison Analysis (SCAN) System
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 134506)
  AUTHORS   Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M.,
            Kadner,K., Miguel,T., Miller,C., Pitluck,S., Pollard,M.,
            Rojeski,H., Subramanian,S. and Martin,C.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-OCT-1998) Human Genome Center, DOE Joint Genome
            Institute, Lawrence Berkeley National Laboratory, MS 74-157,
            Berkeley, CA 94720, U.S.A.
REFERENCE   4  (bases 1 to 134506)
  AUTHORS   Ricke,D.O.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-OCT-1998) Los Alamos National Laboratory, DOE Joint
            Genome Institute, TA43, HRL-1, LS-3, MS M888, Los Alamos, NM 87545,
            USA
REFERENCE   5  (bases 1 to 134506)
  AUTHORS   Ricke,D.O.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-OCT-1998) Los Alamos National Laboratory, DOE Joint
            Genome Institute, TA43, HRL-1, LS-3, MS M888, Los Alamos, NM 87545,
            USA
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            DOE Joint Genome Institute.
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Query Match 69.9%; Score 1177.2; DB 9; Length 134506;
Best Local Similarity 99.6%; Pred. No. 4.8e-231;
Matches 1191; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

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Qy       482 CGCAGGGTCTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTGG 541
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Db    111123 CCCAGGGTCTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTGG 111064

Qy       542 GAGACTTGTGCAAAGGACTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 601
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Db    111063 GAGACTTGTGCAAAGGACTTTGCAGATT--AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 111006

Qy       602 AAAAAAAAAAAAGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGAA 661
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RESULT 10
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LOCUS       AC011428               79970 bp    DNA     linear   HTG 15-NOV-2000
DEFINITION  Homo sapiens chromosome 5 clone XXp1-380H11, WORKING DRAFT
            SEQUENCE, 4 unordered pieces.
ACCESSION   AC011428
VERSION     AC011428.3  GI:11178060
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 79970)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Sequencing of Human Chromosome 5
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 79970)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-OCT-1999) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT     On Nov 15, 2000 this sequence version replaced gi:6604400.
            -------Genome Center
            Center: Joint Genome Institute
            Center Code: JGI
            Web site: http://www.jgi.doe.gov
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            Project Information
            Center Project Name: 1189149, H122
            Center clone name: XXp1-380H11
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            Summary Statistics
            Consensus quality: 76910 bases at least Q40
            Consensus quality: 78432 bases at least Q30
            Consensus quality: 78894 bases at least Q20
            Estimated insert size: 72000; pulse field gel estimation
            Estimated insert size: 79670; sum-of-contigs estimation
            Quality coverage:  7.19 in Q20 bases; pulse field gel estimation
            Quality coverage:  6.49 in Q20 bases; sum-of-contigs estimation.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 4 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
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            *     3225     3324: gap of unknown length
            *     3325    13887: contig of 10563 bp in length
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FEATURES             Location/Qualifiers
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ORIGIN

  Query Match           69.8%;  Score 1175.6;  DB 2;  Length 79970;
  Best Local Similarity   99.5%;  Pred. No. 9.4e-231;
  Matches 1190;  Conservative    0;  Mismatches    4;  Indels    2;  Gaps    1;

Qy         482 CGCAGGGTCTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTGG 541

Db       18644 CCCAGGGTCTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTGG 18585

Qy         542 GAGACTTGTGCAAAGGACTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 601

Db       18584 GAGACTTGTGCAAAGGACTTTGCAGATT--AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 18527

Qy         602 AAAAAAAAAAAAAGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGAA 661

Db       18526 AAAAAAAAAAAAAGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGAA 18467

Qy         662 GCACTTTTTACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGAT 721

Db       18466 GCACTTTTTACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGAT 18407

Qy         722 GGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTTATCAAAAAGGG 781

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Qy         782 GAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTAT 841

Db       18346 GAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTAT 18287

Qy         842 ACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTGC 901

Db       18286 ACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTGC 18227

Qy         902 AGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCACA 961

Db       18226 AGTATTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCACA 18167

Qy         962 GCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTGG 1021

Db       18166 GCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTGG 18107

Qy        1022 CCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAAG 1081

Db       18106 CCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAAG 18047

Qy        1082 TTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGAA 1141

Db       18046 TTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGAA 17987

Qy        1142 ACATTTCCAAGATCCTGTGATGGCGAGACAAATGATCCTTAAAGAAGGTGTGGGGTCTTT 1201

Db       17986 ACATTTCCAAGATCCTGTGATGGCGAGACAAATGATCCTTAAAGAAGGTGTGGGGTCTTT 17927

Qy        1202 CCCAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATATTTAATGCTTCAGAAGCATGT 1261

Db       17926 CCCAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATATTTAATGCTTCAGAAGCATGT 17867

Qy        1262 GAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATATGAATACAT 1321

Db       17866 GAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATATGAATACAT 17807

Qy        1322 GCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGTT 1381

Db       17806 GCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGTT 17747

Qy        1382 TCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATATTTGTGATTCCCCATG 1441

Db       17746 TCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATATTTGTGATTCCCCATG 17687
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Qy       1442 TAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGATGACCATGCGCCCT 1501
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      17686 TAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGATGACCATGCGCCCT 17627

Qy       1502 TTCCTCTGTACATATACCCTTAAGAACGCCCCCTCCACACACTGCCCCCCAGTATATGCC 1561
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      17626 TTCCTCTGTACATATACCCTTAAGAACGCCCCCTCCACACACTGCCCCCCAGTATATGCC 17567

Qy       1562 GCATTGTACTGCTGTGTTATATGCTATGTACATGTCAGAAACCATTAGCATTGCATGCAG 1621
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      17566 GCATTGTACTGCTGTGTTATATGCTATGTACATGTCAGAAACCATTAGCATTGCATGCAG 17507

Qy       1622 GTTTCATATTCTTTCTAAGATGGAAAGTAATAAAATATATTTGAAATGTAAAAAAA 1677
             ||||||||||||||||||||||||||||||||||||||||||||||||||||  ||||
Db      17506 GTTTCATATTCTTTCTAAGATGGAAAGTAATAAAATATATTTGAAATGTACCAAAA 17451
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RESULT 11
AC009017/c

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LOCUS       AC009017               159420 bp    DNA     linear   HTG 20-APR-2001
DEFINITION  Homo sapiens chromosome 5 clone XXp1-929G6, WORKING DRAFT SEQUENCE,
            26 unordered pieces.
ACCESSION   AC009017
VERSION     AC009017.4  GI:13699469
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 159420)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Sequencing of Human Chromosome 5
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 159420)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT     On Apr 20, 2001 this sequence version replaced gi:11178048.
            -------Genome Center
            Center: Joint Genome Institute
            Center Code: JGI
            Web site: http://www.jgi.doe.gov
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            Project Information
            Center Project Name: 1189133, H51
            Center clone name: XXp1-929G6
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            Summary Statistics
            Consensus quality: 142845 bases at least Q40
            Consensus quality: 150910 bases at least Q30
            Consensus quality: 152756 bases at least Q20
            Estimated insert size: 80000; pulse field gel estimation
            Estimated insert size: 156920; sum-of-contigs estimation
            Quality coverage:  8.41 in Q20 bases; pulse field gel estimation
            Quality coverage:  4.29 in Q20 bases; sum-of-contigs estimation.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 26 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     1423: contig of 1423 bp in length
            *     1424     1523: gap of unknown length
            *     1524     3066: contig of 1543 bp in length
            *     3067     3166: gap of unknown length
            *     3167     5629: contig of 2463 bp in length
            *     5630     5729: gap of unknown length
            *     5730     6997: contig of 1268 bp in length
            *     6998     7097: gap of unknown length
            *     7098     9214: contig of 2117 bp in length
            *     9215     9314: gap of unknown length
            *     9315    11813: contig of 2499 bp in length
            *    11814    11913: gap of unknown length
            *    11914    14718: contig of 2805 bp in length
            *    14719    14818: gap of unknown length
            *    14819    17174: contig of 2356 bp in length
            *    17175    17274: gap of unknown length
            *    17275    19710: contig of 2436 bp in length
            *    19711    19810: gap of unknown length
            *    19811    21678: contig of 1868 bp in length
            *    21679    21778: gap of unknown length
            *    21779    26021: contig of 4243 bp in length
            *    26022    26121: gap of unknown length
            *    26122    29609: contig of 3488 bp in length
            *    29610    29709: gap of unknown length
            *    29710    33196: contig of 3487 bp in length
            *    33197    33296: gap of unknown length
            *    33297    36995: contig of 3699 bp in length
            *    36996    37095: gap of unknown length
            *    37096    40646: contig of 3551 bp in length
            *    40647    40746: gap of unknown length
            *    40747    45044: contig of 4298 bp in length
            *    45045    45144: gap of unknown length
            *    45145    52148: contig of 7004 bp in length
            *    52149    52248: gap of unknown length
            *    52249    57686: contig of 5438 bp in length
            *    57687    57786: gap of unknown length
            *    57787    66113: contig of 8327 bp in length
            *    66114    66213: gap of unknown length
            *    66214    75538: contig of 9325 bp in length
            *    75539    75638: gap of unknown length
            *    75639    82249: contig of 6611 bp in length
            *    82250    82349: gap of unknown length
            *    82350    95465: contig of 13116 bp in length
            *    95466    95565: gap of unknown length
            *    95566   110942: contig of 15377 bp in length
            *   110943   111042: gap of unknown length
            *   111043   127290: contig of 16248 bp in length
            *   127291   127390: gap of unknown length
            *   127391   143681: contig of 16291 bp in length
            *   143682   143781: gap of unknown length
            *   143782   159420: contig of 15639 bp in length.
FEATURES             Location/Qualifiers
     source          1. .159420
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="5"
                     /clone="XXp1-929G6"
ORIGIN
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  Query Match           69.8%;  Score 1175.6;  DB 2;  Length 159420;
  Best Local Similarity   99.5%;  Pred. No. 1.1e-230;
  Matches 1190;  Conservative    0;  Mismatches    4;  Indels    2;  Gaps    1;

Qy        482 CGCAGGGTCTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTGG 541
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     152395 CCCAGGGTCTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTGG 152336

Qy        542 GAGACTTGTGCAAAGGACTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 601
              |||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||
Db     152335 GAGACTTGTGCAAAGGACTTTGCAGATT--AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 152278

Qy        602 AAAAAAAAAAAAGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGAA 661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     152277 AAAAAAAAAAAAGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGAA 152218

Qy        662 GCACTTTTTACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGAT 721
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     152217 GCACTTTTTACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGAT 152158

Qy        722 GGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGGG 781
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                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     152157 GGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGGG 152098

Qy        782 GAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTAT 841
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     152097 GAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTAT 152038

Qy        842 ACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTGC 901
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     152037 ACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTGC 151978

Qy        902 AGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCACA 961
                ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     151977 AGTATTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCACA 151918

Qy        962 GCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTGG 1021
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     151917 GCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTGG 151858

Qy       1022 CCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAAG 1081
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     151857 CCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAAG 151798

Qy       1082 TTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGAA 1141
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     151797 TTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGAA 151738

Qy       1142 ACATTTCCAAGATCCTGTGATGGCGAGACAAATGATCCTTAAAGAAGGTGTGGGGTCTTT 1201
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     151737 ACATTTCCAAGATCCTGTGATGGCGAGACAAATGATCCTTAAAGAAGGTGTGGGGTCTTT 151678

Qy       1202 CCCAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATATTTAATGCTTCAGAAGCATGT 1261
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     151677 CCCAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATATTTAATGCTTCAGAAGCATGT 151618

Qy       1262 GAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATATGAATACAT 1321
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     151617 GAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATATGAATACAT 151558

Qy       1322 GCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGTT 1381
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     151557 GCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGTT 151498

Qy       1382 TCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATATTTGTGATTCCCCATG 1441
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     151497 TCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATATTTGTGATTCCCCATG 151438

Qy       1442 TAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGATGACCATGCGCCCT 1501
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     151437 TAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGATGACCATGCGCCCT 151378

Qy       1502 TTCCTCTGTACATATACCCTTAAGAACGCCCCCTCCACACACTGCCCCCCAGTATATGCC 1561
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     151377 TTCCTCTGTACATATACCCTTAAGAACGCCCCCTCCACACACTGCCCCCCAGTATATGCC 151318

Qy       1562 GCATTGTACTGCTGTGTTATATGCTATGTACATGTCAGAAACCATTAGCATTGCATGCAG 1621
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     151317 GCATTGTACTGCTGTGTTATATGCTATGTACATGTCAGAAACCATTAGCATTGCATGCAG 151258

Qy       1622 GTTTCATATTCTTTCTAAGATGGAAAGTAATAAAATATATTTGAAATGTAAAAAAA 1677
                |||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||
Db     151257 GTTTCATATTCTTTCTAAGATGGAAAGTAATAAAATATATTTGAAATGTACCAAAA 151202
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RESULT 12
AC063981/c
LOCUS       AC063981               81811 bp    DNA     linear   HTG 02-SEP-2000
DEFINITION  Homo sapiens chromosome 5 clone XXp1-766F5, WORKING DRAFT SEQUENCE,
            11 ordered pieces.
ACCESSION   AC063981
VERSION     AC063981.2  GI:9964804
KEYWORDS    HTG; HTGS_PHASE2; HTGS_DRAFT.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 81811)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Sequencing of Human Chromosome 5
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 81811)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-APR-2000) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT     On Sep 2, 2000 this sequence version replaced gi:7636394.
            -------Genome Center
            Center: Joint Genome Institute
            Center Code: JGI
            Web site: http://www.jgi.doe.gov
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            Project Information
            Center Project Name: 1189125, H199
            Center clone name: XXp1-766F5
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            Summary Statistics
            Consensus quality: 74154 bases at least Q40
            Consensus quality: 79224 bases at least Q30
            Consensus quality: 80246 bases at least Q20
            Estimated insert size: 76000; pulse field gel estimation
            Estimated insert size: 81361; sum-of-contigs estimation
            Quality coverage:  5.65 in Q20 bases; pulse field gel estimation
            Quality coverage:  5.28 in Q20 bases; sum-of-contigs estimation.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 11 contigs. Gaps between the contigs
            * are represented as runs of N. The order of the pieces
            * is believed to be correct as given, however the sizes
            * of the gaps between them are based on estimates that have
            * provided by the submittor.
            * This sequence will be replaced
            * by the finished sequence as soon as it is available and
            * the accession number will be preserved.
            *        1     3978: contig of 3978 bp in length
            *     3979     4078: gap of unknown length
            *     4079    42436: contig of 38358 bp in length
            *    42437    42536: gap of unknown length
            *    42537    44222: contig of 1686 bp in length
            *    44223    44322: gap of unknown length
            *    44323    50495: contig of 6173 bp in length
            *    50496    50595: gap of unknown length
            *    50596    51958: contig of 1363 bp in length
            *    51959    52058: gap of unknown length
            *    52059    55493: contig of 3435 bp in length
            *    55494    55593: gap of unknown length
            *    55594    65183: contig of 9590 bp in length
            *    65184    65283: gap of unknown length
            *    65284    69297: contig of 4014 bp in length
            *    69298    69397: gap of unknown length
            *    69398    71766: contig of 2369 bp in length
            *    71767    71866: gap of unknown length
            *    71867    80791: contig of 8925 bp in length
            *    80792    80891: gap of unknown length
            *    80892    81811: contig of 920 bp in length.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="5"
                     /clone="XXp1-766F5"
ORIGIN

  Query Match             69.1%;  Score 1163.6;  DB 2;  Length 81811;
  Best Local Similarity   99.4%;  Pred. No. 2.8e-228;
  Matches 1189;  Conservative    0;  Mismatches    4;  Indels    3;  Gaps    2;
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Qy       482 CGCAGGGTCTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTGG 541
Db     16045 CCCAGGGTCTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTGG 15986

Qy       542 GAGACTTGTGCAAAGGACTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 601
Db     15985 GAGACTTGTGCAAAGGACTTTGCAGATT--AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 15928

Qy       602 AAAAAAAAAAAAGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGAA 661
Db     15927 AAAAAAAAAAAAGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGAA 15868

Qy       662 GCACTTTTTACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGAT 721
Db     15867 GCACTTTTTACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGAT 15808

Qy       722 GGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTTATCAAAAAGGG 781
Db     15807 GGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTTATCAAAAAGGG 15748

Qy       782 GAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTTGTATTTGTCCATACGTCACTAT 841
Db     15747 GAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTTGTATTTGTCCATACGTCACTAT 15688

Qy       842 ACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTGC 901
Db     15687 ACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTGC 15628

Qy       902 AGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCACA 961
Db     15627 AGTATTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCACA 15568

Qy       962 GCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTGG 1021
Db     15567 GCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTGG 15508

Qy      1022 CCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAAG 1081
Db     15507 CCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAAG 15448

Qy      1082 TTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGAA 1141
Db     15447 TTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGAA 15388

Qy      1142 ACATTTCCAAGATCCTGTGATGGCGAGACAAATGATCCTTAAAGAAGGTGTGGGGTCTTT 1201
Db     15387 ACATTTCCAAGATCCTGTGATGGCGAGACAAATGATCCTTAAAGAAGGTGTGGGGTCTTT 15328

Qy      1202 CCCAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATATTTAATGCTTCAGAAGCATGT 1261
Db     15327 CCCAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATATTTAATGCTTCAGAAGCATGT 15268

Qy      1262 GAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATATGAATACAT 1321
Db     15267 GAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATATGAATACAT 15208

Qy      1322 GCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGTT 1381
Db     15207 GCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGTT 15148

Qy      1382 TCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATATTTGTGATTCCCCATG 1441
Db     15147 TCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATATTTGTGATTCCCCATG 15088

Qy      1442 TAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGATGACCATGCGCCCT 1501
Db     15087 TAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGATGACCATGCGCCCT 15028

Qy      1502 TTCCTCTGTACATATACCCTTAAGAACGCCCCCTCCACACACTGCCCCCCAGTATATGCC 1561
Db     15027 TTCCTCTGTACATATACCCTTAAGAACGCCCCCTCCACACACTGCCCCCCAGTATATGCC 14968

Qy      1562 GCATTGTACTGCTGTGTTTATATGCTATGTACATGTCAGAAACCATTAGCATTGCATGCAG 1621
Db     14967 GCATTGTACTGCTGTGTTTATATGCTATGTACATGTCAGAAACCATTAGCA-TGCATGCAG 14909

Qy      1622 GTTTCATATTCTTTCTAAGATGGAAAGTAATAAAATATATTTGAAATGTAAAAAAA 1677
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RESULT 13
AR400615
LOCUS AR400615 1630 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 59 from patent US 6620923.
ACCESSION AR400615
VERSION AR400615.1 GI:40144431
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1630)
AUTHORS Specht,T., Hinzmann,B., Schmitt,A., Pilarsky,C., Dahl,E. and Rosenthal,A.
TITLE Human nucleic acid sequences from endometrial tumor tissue
JOURNAL Patent: US 6620923-A 59 16-SEP-2003;
FEATURES Location/Qualifiers
source 1. .1630
/organism="unknown"
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Query Match 64.8%; Score 1092.2; DB 6; Length 1630;
Best Local Similarity 99.7%; Pred. No. 6.9e-214;
Matches 1094; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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RESULT 14
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DEFINITION  Sequence 59 from Patent WO9954461.
ACCESSION   AX013119
VERSION     AX013119.1  GI:10040285
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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REFERENCE   1
  AUTHORS   Schmitt,A., Specht,T., Dahl,E., Hinzmann,B., Rosenthal,A. and
            Pilarsky,C.
  TITLE     Human nucleic acid sequences of endometrium tumour tissue
  JOURNAL   Patent: WO 9954461-A 59 28-OCT-1999;
            SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN
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FEATURES             Location/Qualifiers
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Query Match 64.8%; Score 1092.2; DB 6; Length 1630;
Best Local Similarity 99.7%; Pred. No. 6.9e-214;
Matches 1094; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy        575 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCCTTTCTTTCTCACAGGCAT 634
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Qy       1655 AATATATTTGAAATGTA 1671
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Db       1612 AATATATTTGAAATGTA 1628
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LOCUS       BD206300               1630 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Human nucleic acid sequence originating in endometrial tumor
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ACCESSION   BD206300
VERSION     BD206300.1  GI:33016070
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1630)
  AUTHORS   Specht,T., Hinzmann,B., Schmitt,A., Pilarsky,C., Dahl,E. and
            Rosenthal,A.
  TITLE     Human nucleic acid sequence originating in endometrial tumor tissue
  JOURNAL   Patent: JP 2002532055-A 59 02-OCT-2002;
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            PD   02-OCT-2002
            PF   15-APR-1999 JP 2000544793
            PR   17-APR-1998 DE 198 17 948.0
            PI   THOMAS SPECHT,BERND HINZMANN,ARMIN SCHMITT,CHRISTIAN PILARSKY,
            PI   EDGAR DAHL,
            PI   ANDRE ROSENTHAL
            PC   C12N15/09,A61K38/00,A61K48/00,C07K14/47,C07K16/18,C12N5/10, PC
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Query Match 64.8%; Score 1092.2; DB 6; Length 1630;
Best Local Similarity 99.7%; Pred. No. 6.9e-214;
Matches 1094; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy        575 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCCTTTCTTTCTCACAGGCAT 634
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GenCore version 5.1.6

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	5	727.2	43.2	1663	4	US-09-312-283C-370	Sequence 370, App
	6	727.2	43.2	1663	4	US-09-312-283C-416	Sequence 416, App
	7	448	26.6	764	3	US-09-188-930-263	Sequence 263, App
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	26	56.2	3.3	231	4	US-09-621-976-16317	Sequence 16317, A
	27	56.2	3.3	242	4	US-09-621-976-16320	Sequence 16320, A
	28	56.2	3.3	242	4	US-09-621-976-16324	Sequence 16324, A
	29	55.2	3.3	289	3	US-09-007-005-17	Sequence 17, Appl
	30	55.2	3.3	289	3	US-09-244-796-17	Sequence 17, Appl
	31	55.2	3.3	2230	3	US-08-378-313-24	Sequence 24, Appl
c	32	54.8	3.3	260	2	US-08-520-678A-29	Sequence 29, Appl
c	33	54.8	3.3	260	3	US-08-897-126-29	Sequence 29, Appl
	34	54.6	3.2	1804	2	US-08-504-459-5	Sequence 5, Appli
	35	54.4	3.2	1771	4	US-09-907-794A-158	Sequence 158, App
	36	54.4	3.2	1771	4	US-09-866-028-36	Sequence 36, Appl
	37	54.4	3.2	1771	4	US-09-905-125A-158	Sequence 158, App
	38	54.4	3.2	1771	4	US-09-902-775A-158	Sequence 158, App
	39	54	3.2	282	4	US-09-621-976-18648	Sequence 18648, A
c	40	53.6	3.2	63000	4	US-09-780-172-18	Sequence 18, Appl
	41	53.4	3.2	335	4	US-09-621-976-16038	Sequence 16038, A
	42	53.4	3.2	1279	3	US-09-248-335-25	Sequence 25, Appl
	43	53.4	3.2	3214	1	US-08-484-105-17	Sequence 17, Appl
	44	53.4	3.2	3214	1	US-08-484-106-17	Sequence 17, Appl
	45	53	3.1	1210	4	US-09-443-041A-29	Sequence 29, Appl

ALIGNMENTS

```
RESULT 1
US-09-023-655-225
; Sequence 225, Application US/09023655
; Patent No. 6607879
;  GENERAL INFORMATION:
;    APPLICANT:  Cocks, Benjamin G.
;    APPLICANT:  Susan G. Stuart
;    APPLICANT:  Jeffrey J. Seilhamer
;    TITLE OF INVENTION:  COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  1508
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
;      STREET:  3174 PORTER DRIVE
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/023,655
;      FILING DATE:  HEREWITH
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Zeller, Karen J.
;      REGISTRATION NUMBER:  37,071
;      REFERENCE/DOCKET NUMBER:  PA-0001 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 855-0555
;      TELEFAX:  (650) 845-4166
;  INFORMATION FOR SEQ ID NO:  225:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1865 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  BRSTNOT03
;      CLONE:  1000787
US-09-023-655-225

  Query Match          86.0%;  Score 1449.2;  DB 4;  Length 1865;
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Best Local Similarity   94.6%;  Pred. No. 0;
Matches 1604;  Conservative    0;  Mismatches   57;  Indels   34;  Gaps   11;

Qy          1 GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGG 60
Db        172 GCGGAGACAAGCGCAGAGCGCAGCCNACGGCCACAGACAGCCCTGGGCATCCACCGACGG 231

Qy         61 CGCAGCCGGAGCCAGCAGAGCCGGAAGGCGC-GCCCCGGGCAGAGAAAGCCGAGCAGAGC 119
Db        232 CGCA-CNGNGGCCAGCAGAGCCGGAAGGCGCGGCCCCGGGCAGAGAAAGCCGAGCAGAGC 290

Qy        120 TGGGTGGCGTCTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCC 179
Db        291 TGGGTGGCGTCTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCC 350

Qy        180 CACGCCGCGCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGC 239
Db        351 CACGCCGCGCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCNNNNNNNNNNNNNNNNN 410

Qy        240 TGGCGCTGTACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCA 299
Db        411 NNNNNNNNTACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCA 470

Qy        300 AGATCCGCTACAGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGG 359
Db        471 AGATCCGCTACAGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGG 530

Qy        360 AGAAGATGGTTATCATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCC 419
Db        531 AGAAGATGGTTATCATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCC 590

Qy        420 TGCACCCCAAGCTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGA 479
Db        591 TGCACCCCAAGCTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGA 650

Qy        480 AGCGCAGGGTCTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTT 539
Db        651 AGCGCAGGGTCTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTT 710

Qy        540 GGGAGACTTGTGCAAAGGACTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 599
Db        711 GGGAGACTTGTGCAAAGGACTTTGCAGATT--------------------AAANNNNAA 749

Qy        600 AAAAAAAAAAAAAAGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATG 659
Db        750 NATNAAANNAANNNGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATG 809

Qy        660 AAGCACTTTTTA-CCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCA 718
Db        810 AAGCACTTTTTACCCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCA 869

Qy        719 GATGGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTATCAAAAA 778
Db        870 GATGGGAGACCCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTTATCAAAAA 929

Qy        779 GGGGAAAACTCATGCCTTTCCTTTTT-AAAAAATGCTTTTTTGTATTTGTCCATACGTCA 837
Db        930 GGGGAAAACTCATGCCTTTCCTTTTTAAAAAAATGCTTTTTTGTATTTGTCCATACGTCA 989

Qy        838 CTATACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCA 897
Db        990 CTATACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCA 1049

Qy        898 TTGCAGTGTTGCTCCATTCCTAGCTTGGGAAGC-TTCCGCTTAGAGGTCCTGGCGCCTCG 956
Db       1050 TTGCAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTTCCGCTTAGAGGTCCTGGCGCCTCG 1109

Qy        957 GCACAGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCAC 1016
Db       1110 GCACAGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCAC 1169

Qy       1017 AGTGGCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAAC 1076
Db       1170 AGTGGCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAAC 1229

Qy       1077 TCAAGTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCT 1136
Db       1230 TCAAGTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACGGCCT 1289

Qy       1137 --AGGAAACATTTCCAA-GATCCTGTGATGGCGAGACAAATGATCCTTAAA-GAAGGTGT 1192
Db       1290 TAGGGAAACATTTCCAAGGATCCTGTGATGGCGAGACAAATGATCCTTAAAGGAAGGTGT 1349

Qy       1193 GGGGTCTTT--CCCAACCTGAGGATTTCTGAAAGGTT--CACAGGTTCAATATTTAATGC 1248
Db       1350 GGGGTCTTTTCCCAACCTGAGGATTTCTGAAAGGTTTCACAGGTTTCAATATTTAATGC 1409

Qy       1249 TTCAGAAGCATGTGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAA 1308
Db       1410 TTCAGAAGCATGTGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAA 1469

Qy       1309 TATATGAATACATGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACC 1368
Db       1470 TATATGAATACATGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACC 1529

Qy       1369 TTCAAAGCATGTTTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATATTT 1428
Db       1530 TTCAAAGCATGTTTCTTTCCCTCACCACAACAGGACATGCAGTACTAAAGCAATATATTT 1589

Qy       1429 GTGATTCCCCATGTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGAT 1488
Db       1590 GTGATTCCCCATGTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGAT 1649

Qy       1489 GACCATGCGCCCTTTCCTCTGTACATATACCCTTAAGAACGCCCCCTCCACACACTGCCC 1548
Db       1650 GACCATGCGCCCTTTCCTCTGTACATATACCCTTAAGAACGCCCCCTCCACACACTGCCC 1709

Qy       1549 CCCAGTATATGCCGCATTGTACTGCTGTGTTATATGCTATGTACATGTCAGAAACCATTA 1608
Db       1710 CCCAGTATATGCCGCATTGTACTGCTGTGTTATATGCTATGTACATGTCAGAAACCATTA 1769

Qy       1609 GCATTGCATGCAGGTTTCATATTCTTTCTAAGATGGAAAGTAATAAAATATATTTGAAAT 1668
Db       1770 GCATTGCATGCAGGTTTCATATTCTTTCTAAGATGGAAAGTAATAAAATATATTTGAAAT 1829

Qy       1669 GTAAAAAAAAAAAA 1683
Db       1830 GTAAAAAAAAAAAA 1844

RESULT 2
US-09-673-395A-59
; Sequence 59, Application US/09673395A
; Patent No. 6620923
; GENERAL INFORMATION:
;  APPLICANT: SPECHT, THOMAS
;  APPLICANT:  HINZMANN, BERND
;  APPLICANT:  SCHMITT, ARMIN
;  APPLICANT:  PILARSKY, CHRISTIAN
;  APPLICANT:  DAHL, EDGAR
;  APPLICANT:  ROSENTHAL, ANDRE
;  TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE
;  FILE REFERENCE: ALBRE-12
;  CURRENT APPLICATION NUMBER: US/09/673,395A
;  CURRENT FILING DATE:  2000-10-17
;  NUMBER OF SEQ ID NOS: 637
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
;   LENGTH: 1630
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-673-395A-59

  Query Match             64.8%;  Score 1092.2;  DB 4;  Length 1630;
  Best Local Similarity   99.7%;  Pred. No. 5.5e-247;
  Matches 1094;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;
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Qy       575 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCCTTTCTTTCTCACAGGCAT 634
Db       532 ACAAATACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCCTTTCTTTCTCACAGGCAT 591

Qy       635 AAGACACAAATTATATATTGTTATGAAGCACTTTTTACCAACGGTCAGTTTTTACATTTT 694
Db       592 AAGACACAAATTATATATTGTTATGAAGCACTTTTTACCAACGGTCAGTTTTTACATTTT 651

Qy       695 ATAGCTGCGTGCGAAAGGCTTCCAGATGGGAGACCCATCTCTCTTGTGCTCCAGACTTCA 754
Db       652 ATAGCTGCGTGCGAAAGGCTTCCAGATGGGAGACCCATCTCTCTTGTGCTCCAGACTTCA 711

Qy       755 TCACAGGCTGCTTTTTATCAAAAAGGGGAAAACTCATGCCTTTCCTTTTTAAAAAATGCT 814
Db       712 TCACAGGCTGCTTTTTATCAAAAAGGGGAAAACTCATGCCTTTCCTTTTTAAAAAATGCT 771

Qy       815 TTTTTGTATTTGTCCATACGTCACTATACATCTGAGCTTTATAAGCGCCCGGGAGGAACA 874
Db       772 TTTTTGTATTTGTCCATACGTCACTATACATCTGAGCTTTATAAGCGCCCGGGAGGAACA 831

Qy       875 ATGAGCTTGGTGGACACATTTCATTGCAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCC 934
Db       832 ATGAGCTTGGTGGACACATTTCATTGCAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCC 891

Qy       935 GCTTAGAGGTCCTGGCGCCTCGGCACAGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGT 994
Db       892 GCTTAGAGGTCCTGGCGCCTCGGCACAGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGT 951

Qy       995 CACAGCCTCAGTGTGACTCCACAGTGGCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCT 1054
Db       952 CACAGCCTCAGTGTGACTCCACAGTGGCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCT 1011

Qy      1055 CTGCATCTGTTCTCTGAGGAACTCAAGTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCC 1114
Db      1012 CTGCATCTGTTCTCTGAGGAACTCAAGTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCC 1071

Qy      1115 CTGGTTAATTTTTACACACCCTAGGAAACATTTCCAAGATCCTGTGATGGCGAGACAAAT 1174
Db      1072 CTGGTTAATTTTTACACACCCTAGGAAACATTTCCAAGATCCTGTGATGGCGAGACAAAT 1131

Qy      1175 GATCCTTAAAGAAGGTGTGGGGTCTTTCCCAACCTGAGGATTTCTGAAAGGTTCACAGGT 1234
Db      1132 GATCCTTAAAGAAGGTGTGGGGTCTTTCCCAACCTGAGGATTTCTGAAAGGTTCACAGGT 1191

Qy      1235 TCAATATTTAATGCTTCAGAAGCATGTGAGGTTCCCAACACTGTCAGCAAAAACCTTAGG 1294
Db      1192 TCAATATTTAATGCTTCAGAAGCATGTGAGGTTCCCAACACTGTCAGCAAAAACCTTAGG 1251

Qy      1295 AGAAAACTTAAAAATATATGAATACATGCGCAATACACAGCTACAGACACACATTCTGTT 1354
Db      1252 AGAAAACTTAAAAATATATGAATACATGCGCAATACACAGCTACAGACACACATTCTGTT 1311

Qy      1355 GACAAGGGAAAACCTTCAAAGCATGTTTCTTTCCCTCACCACAACAGAACATGCAGTACT 1414
Db      1312 GACAAGGGAAAACCTTCAAAGCATGTTTCTTTCCCTCACCACAACAGAACATGCAGTACT 1371

Qy      1415 AAAGCAATATATTTGTGATTCCCCATGTAATTCTTCAATGTTAAACAGTGCAGTCCTCTT 1474
Db      1372 AAAGCAATATATTTGTGATTCCCCATGTAATTCTTCAATGTTAAACAGTGCAGTCCTCTT 1431

Qy      1475 TCGAAAGCTAAGATGACCATGCGCCCTTTCCTCTGTACATATACCCTTAAGAACGCCCCC 1534
Db      1432 TCGAAAGCTAAGATGACCATGCGCCCTTTCCTCTGTACATATACCCTTAAGAACGCCCCC 1491

Qy      1535 TCCACACACTGCCCCCCAGTATATGCCGCATTGTACTGCTGTGTTATATGCTATGTACAT 1594
Db      1492 TCCACACACTGCCCCCCAGTATATGCCGCATTGTACTGCTGTGTTATATGCTATGTACAT 1551

Qy      1595 GTCAGAAACCATTAGCATTGCATGCAGGTTTCATATTCTTTCTAAGATGGAAAGTAATAA 1654
Db      1552 GTCAGAAACCATTAGCATTGCATGCAGGTTTCATATTCTTTCTAAGATGGAAAGTAATAA 1611

Qy      1655 AATATATTTGAAATGTA 1671
Db      1612 AATATATTTGAAATGTA 1628
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RESULT 3
US-09-673-395A-541
; Sequence 541, Application US/09673395A
; Patent No. 6620923
; GENERAL INFORMATION:
; APPLICANT: SPECHT, THOMAS
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHMITT, ARMIN
; APPLICANT: PILARSKY, CHRISTIAN
; APPLICANT: DAHL, EDGAR
; APPLICANT: ROSENTHAL, ANDRE
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE
; FILE REFERENCE: ALBRE-12
; CURRENT APPLICATION NUMBER: US/09/673,395A
; CURRENT FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 637
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 541
; LENGTH: 1962
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-673-395A-541

Query Match 57.9%; Score 976.2; DB 4; Length 1962;
Best Local Similarity 99.7%; Pred. No. 1.1e-219;
Matches 978; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       575 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCCTTTCTTTCTCACAGGCAT 634
Db       879 ACAAATACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCCTTTCTTTCTCACAGGCAT 938

Qy       635 AAGACACAAATTATATATTGTTATGAAGCACTTTTTACCAACGGTCAGTTTTTACATTTT 694
Db       939 AAGACACAAATTATATATTGTTATGAAGCACTTTTTACCAACGGTCAGTTTTTACATTTT 998

Qy       695 ATAGCTGCGTGCGAAAGGCTTCCAGATGGGAGACCCATCTCTCTTGTGCTCCAGACTTCA 754
Db       999 ATAGCTGCGTGCGAAAGGCTTCCAGATGGGAGACCCATCTCTCTTGTGCTCCAGACTTCA 1058

Qy       755 TCACAGGCTGCTTTTTATCAAAAAGGGGAAAACTCATGCCTTTCCTTTTTAAAAAATGCT 814
Db      1059 TCACAGGCTGCTTTTTATCAAAAAGGGGAAAACTCATGCCTTTCCTTTTTAAAAAATGCT 1118

Qy       815 TTTTTGTATTTGTCCATACGTCACTATACATCTGAGCTTTATAAGCGCCCGGGAGGAACA 874
Db      1119 TTTTTGTATTTGTCCATACGTCACTATACATCTGAGCTTTATAAGCGCCCGGGAGGAACA 1178

Qy       875 ATGAGCTTGGTGGACACATTTCATTGCAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCC 934
Db      1179 ATGAGCTTGGTGGACACATTTCATTGCAGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCC 1238

Qy       935 GCTTAGAGGTCCTGGCGCCTCGGCACAGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGT 994
Db      1239 GCTTAGAGGTCCTGGCGCCTCGGCACAGCTGCCACGGGCTCTCCTGGGCTTATGGCCGGT 1298

Qy       995 CACAGCCTCAGTGTGACTCCACAGTGGCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCT 1054
Db      1299 CACAGCCTCAGTGTGACTCCACAGTGGCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCT 1358

Qy      1055 CTGCATCTGTTCTCTGAGGAACTCAAGTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCC 1114
Db      1359 CTGCATCTGTTCTCTGAGGAACTCAAGTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCC 1418

Qy      1115 CTGGTTAATTTTTACACACCCTAGGAAACATTTCCAAGATCCTGTGATGGCGAGACAAAT 1174
Db      1419 CTGGTTAATTTTTACACACCCTAGGAAACATTTCCAAGATCCTGTGATGGCGAGACAAAT 1478

Qy      1175 GATCCTTAAAGAAGGTGTGGGGTCTTTCCCAACCTGAGGATTTCTGAAAGGTTCACAGGT 1234
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Db       1479 GATCCTTAAAGAAGGTGTGGGGTCTTTCCCAACCTGAGGATTTCTGAAAGGTTCACAGGT 1538

Qy       1235 TCAATATTTAATGCTTCAGAAGCATGTGAGGTTCCCAACACTGTCAGCAAAAACCTTAGG 1294

Db       1539 TCAATATTTAATGCTTCAGAAGCATGTGAGGTTCCCAACACTGTCAGCAAAAACCTTAGG 1598

Qy       1295 AGAAAACTTAAAAATATATGAATACATGCGCAATACACAGCTACAGACACACATTCTGTT 1354

Db       1599 AGAAAACTTAAAAATATATGAATACATGCGCAATACACAGCTACAGACACACATTCTGTT 1658

Qy       1355 GACAAGGGAAAACCTTCAAAGCATGTTTCTTTCCCTCACCACAACAGAACATGCAGTACT 1414

Db       1659 GACAAGGGAAAACCTTCAAAGCATGTTTCTTTCCCTCACCACAACAGAACATGCAGTACT 1718

Qy       1415 AAAGCAATATATTTGTGATTCCCCATGTAATTCTTCAATGTTAAACAGTGCAGTCCTCTT 1474

Db       1719 AAAGCAATATATTTGTGATTCCCCATGTAATTCTTCAATGTTAAACAGTGCAGTCCTCTT 1778

Qy       1475 TCGAAAGCTAAGATGACCATGCGCCCTTTCCTCTGTACATATACCCTTAAGAACGCCCCC 1534

Db       1779 TCGAAAGCTAAGATGACCATGCGCCCTTTCCTCTGTACATATACCCTTAAGAACGCCCCC 1838

Qy       1535 TCCACACACTGCCCCCCAGTA 1555

Db       1839 TCCACACACTGCCCCCCAGTA 1859
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RESULT 4
US-09-673-395A-541/c
; Sequence 541, Application US/09673395A
; Patent No. 6620923
; GENERAL INFORMATION:
; APPLICANT: SPECHT, THOMAS
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHMITT, ARMIN
; APPLICANT: PILARSKY, CHRISTIAN
; APPLICANT: DAHL, EDGAR
; APPLICANT: ROSENTHAL, ANDRE
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE
; FILE REFERENCE: ALBRE-12
; CURRENT APPLICATION NUMBER: US/09/673,395A
; CURRENT FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 637
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 541
; LENGTH: 1962
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-673-395A-541

Query Match 51.8%; Score 872.6; DB 4; Length 1962;
Best Local Similarity 97.9%; Pred. No. 2.3e-195;
Matches 884; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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Qy        782 GAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTAT 841

Db        924 GAAAGGCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGTATTTGTCCATACGTCACTAT 865

Qy        842 ACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTGC 901

Db        864 ACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTGC 805

Qy        902 AGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCACA 961

Db        804 AGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCACA 745

Qy        962 GCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTGG 1021

Db        744 GCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTGG 685

Qy       1022 CCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAAG 1081

Db        684 CCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAAG 625

Qy       1082 TTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGAA 1141

Db        624 TTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGTTAATTTTTACACACCCTAGGAA 565

Qy       1142 ACATTTCCAAGATCCTGTGATGGCGAGACAAATGATCCTTAAAGAAGGTGTGGGGTCTTT 1201

Db        564 ACATTTCCAAGATCCTGTGATGGCGAGACAAATGATCCTTAAAGAAGGTGTGGGGTCTTT 505

Qy       1202 CCCAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATATTTAATGCTTCAGAAGCATGT 1261

Db        504 CCCAACCTGAGGATTTCTGAAAGGTTCACAGGTTCAATATTTAATGCTTCAGAAGCATGT 445

Qy       1262 GAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATATGAATACAT 1321

Db        444 GAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACTTAAAAATATATGAATACAT 385

Qy       1322 GCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGTT 1381

Db        384 GCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAAAACCTTCAAAGCATGTT 325

Qy       1382 TCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATATTTGTGATTCCCCATG 1441

Db        324 TCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATATTTGTGATTCCCCATG 265

Qy       1442 TAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGATGACCATGCGCCCT 1501

Db        264 TAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGATGACCATGCGCCCT 205

Qy       1502 TTCCTCTGTACATATACCCTTAAGAACGCCCCCTCCACACACTGCCCCCCAGTATATGCC 1561

Db        204 TTCCTCTGTACATATACCCTTAAGAACGCCCCCTCCACACACTGCCCCCCAGTATATGCC 145

Qy       1562 GCATTGTACTGCTGTGTTATATGCTATGTACATGTCAGAAACCATTAGCATTGCATGCAG 1621

Db        144 GCATTGTACTGCTGTGTTATATGCTATGTACATGTCAGAAACCATTAGCATTGCATGCAG 85

Qy       1622 GTTTCATATTCTTTCTAAGATGGAAAGTAATAAAATATATTTGAAATGTAAAAAAAAAAA 1681

Db          84 GTTTCATATTCTTTCTAAGATGGAAAGTAATAAAATATATTTGAAATGTAAAAAAAAAAA 25

Qy       1682 AAA 1684

Db          24 AGA 22
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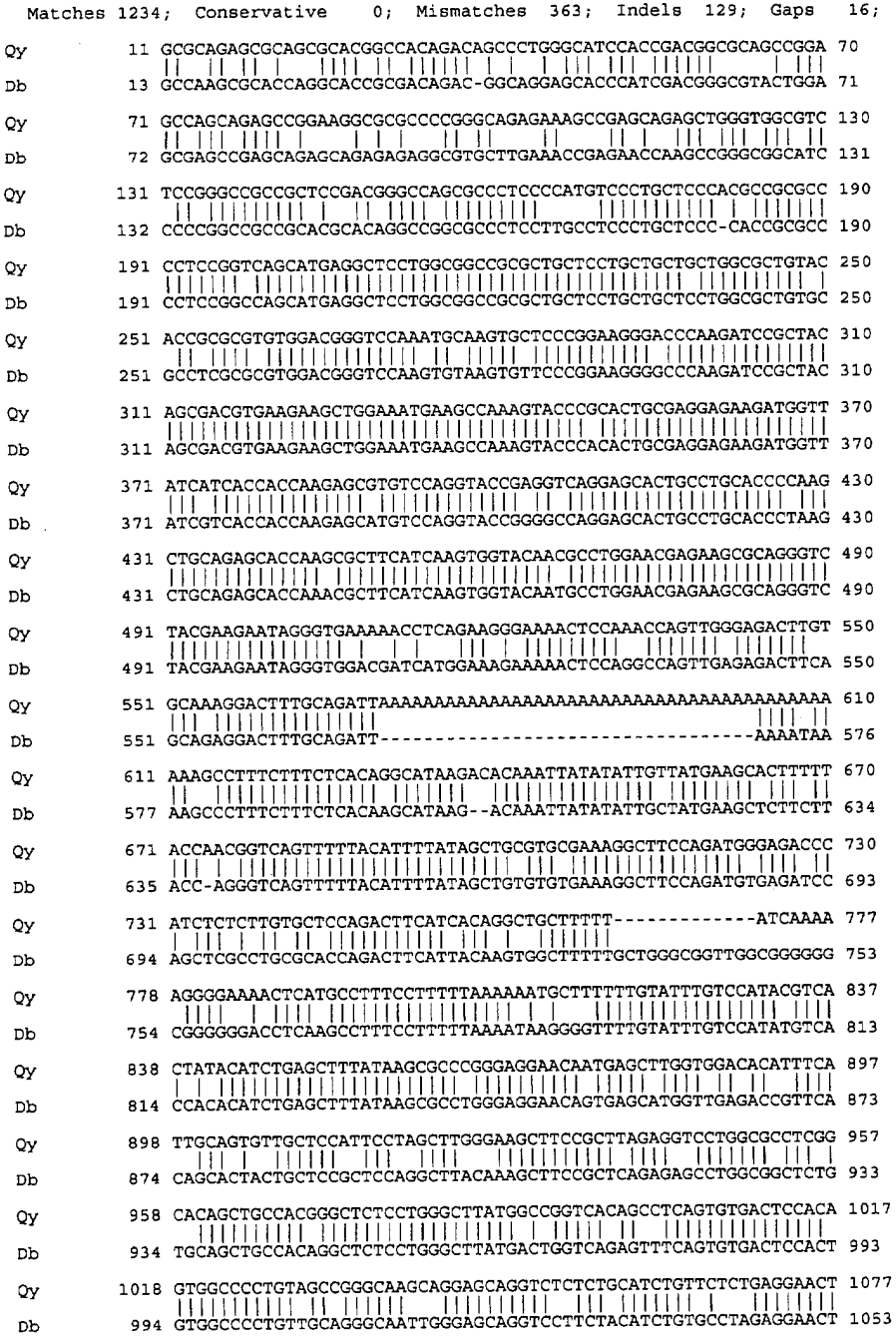
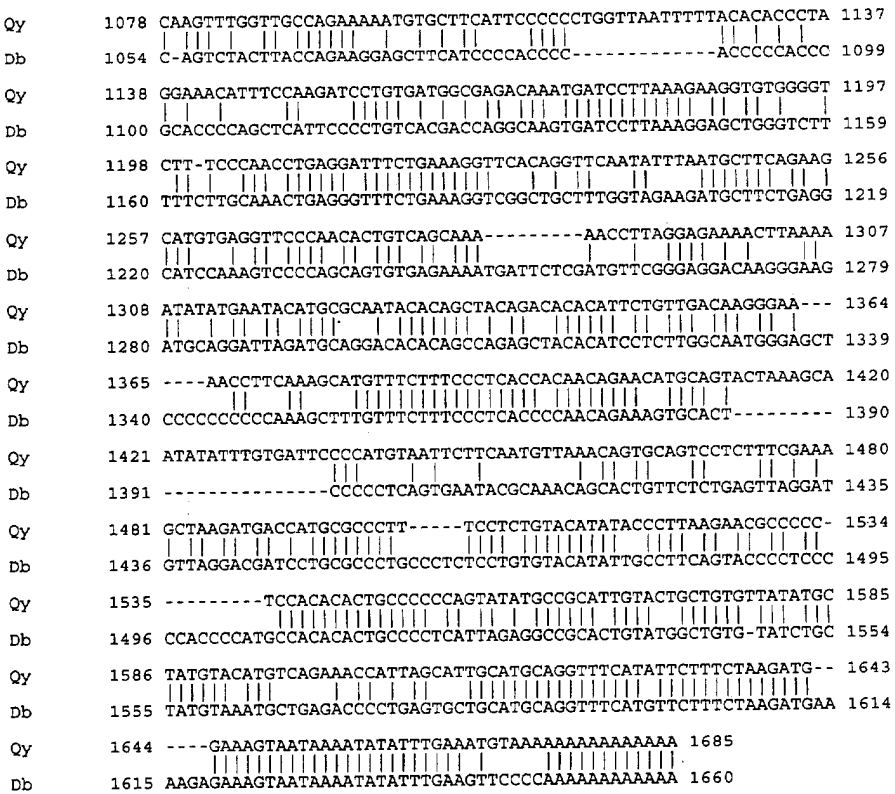
RESULT 5
US-09-312-283C-370
; Sequence 370, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011c2
; CURRENT APPLICATION NUMBER: US/09/312,283C
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 370
; LENGTH: 1663
; TYPE: DNA
; ORGANISM: Mouse
US-09-312-283C-370

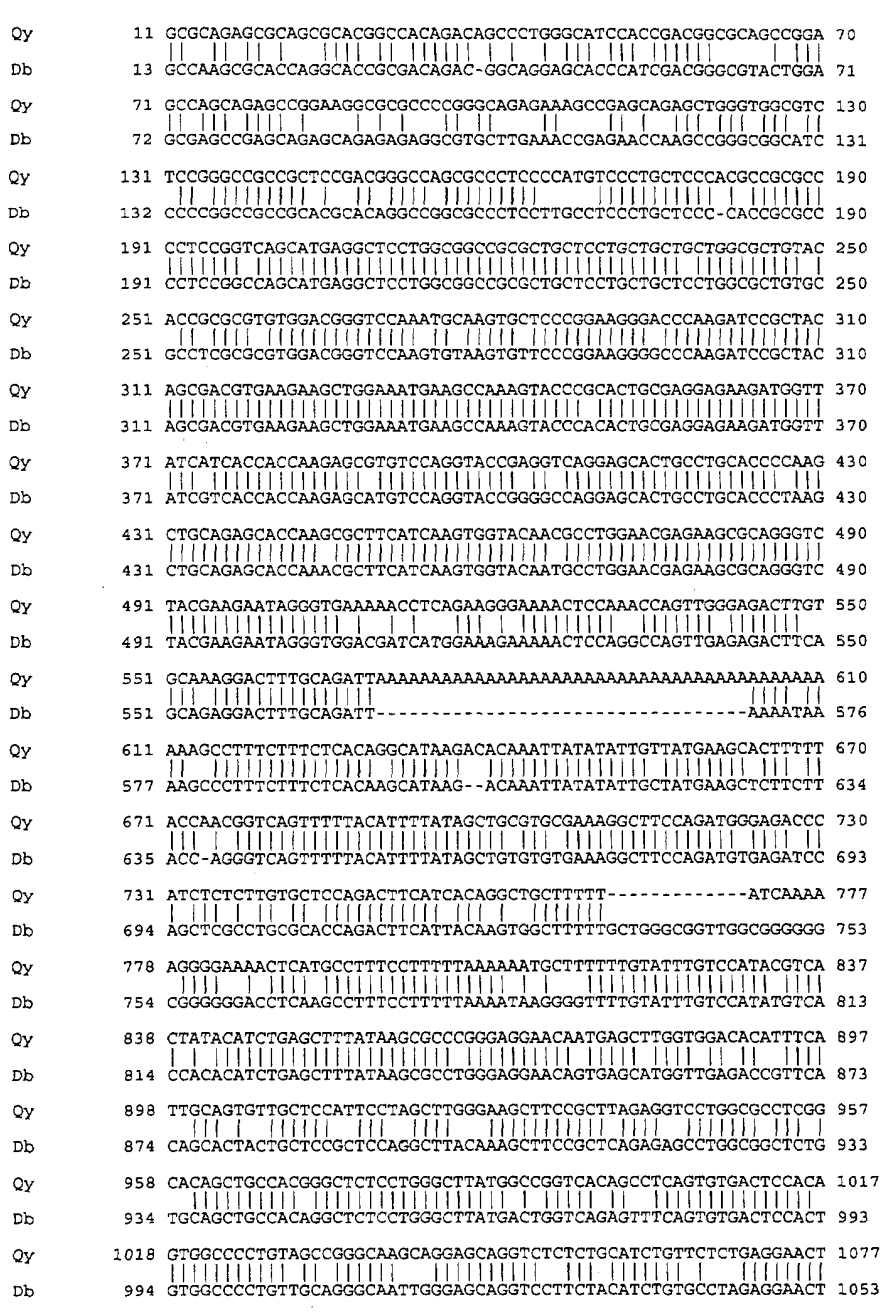
Query Match 43.2%; Score 727.2; DB 4; Length 1663;
Best Local Similarity 71.5%; Pred. No. 2.9e-161;

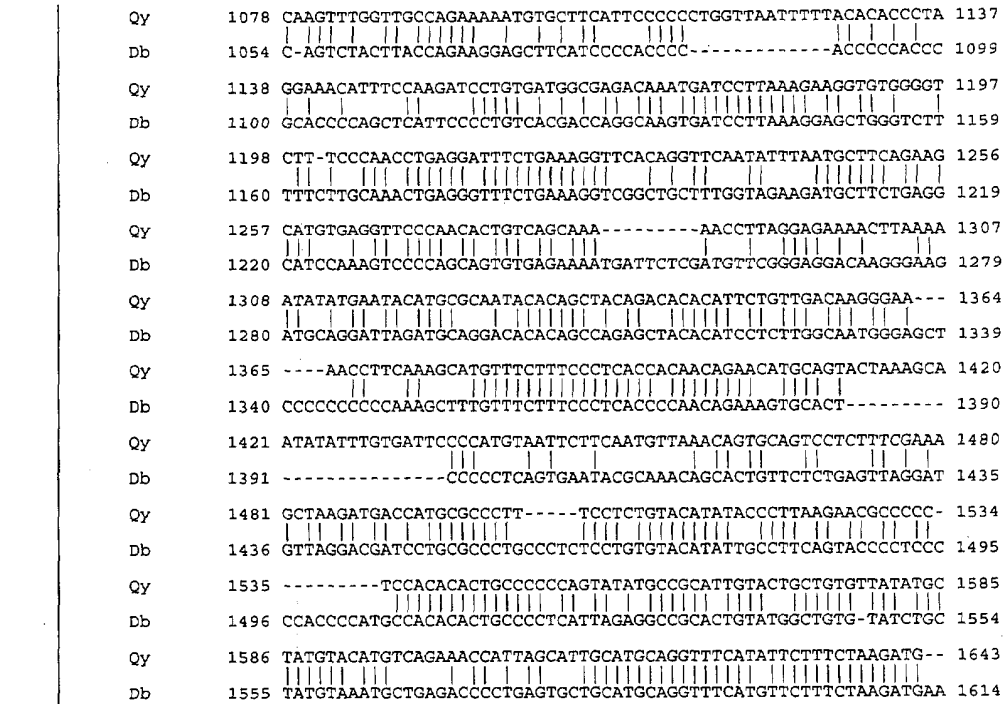




RESULT 6
US-09-312-283C-416
; Sequence 416, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011c2
; CURRENT APPLICATION NUMBER: US/09/312,283C
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 416
; LENGTH: 1663
; TYPE: DNA
; ORGANISM: Mouse
US-09-312-283C-416

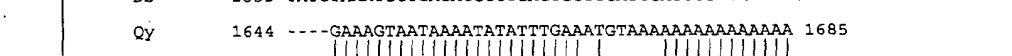
Query Match 43.2%; Score 727.2; DB 4; Length 1663;
Best Local Similarity 71.5%; Pred. No. 2.9e-161;
Matches 1234; Conservative 0; Mismatches 363; Indels 129; Gaps 16;





RESULT 7
US-09-188-930-263
; Sequence 263, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 263
; LENGTH: 764
; TYPE: DNA
; ORGANISM: Mouse
US-09-188-930-263

Query Match 26.6%; Score 448; DB 3; Length 764;
Best Local Similarity 79.7%; Pred. No. 7.6e-96;
Matches 606; Conservative 0; Mismatches 115; Indels 39; Gaps 5;



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Db          13 GCCAAGCGCACCAGGCACCGCGACAGAC-GGCAGGAGCACCCATCGACGGGCGTACTGGA 71

Qy          71 GCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCTGGGTGGCGTC 130

Db          72 GCGAGCCGAGCAGAGCAGAGAGAGGCGTGCTTGAAACCGAGAACCAAGCCGGGCGGCATC 131

Qy         131 TCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCCACGCCGCGCC 190

Db         132 CCCCGGCCGCCGCACGCACAGGCCGGCGCCCTCCTTGCCTCCCTGCTCCC-CACCGCGCC 190

Qy         191 CCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCTGGCGCTGTAC 250

Db         191 CCTCCGGCCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTCCTGGCGCTGTGC 250

Qy         251 ACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAAGATCCGCTAC 310

Db         251 GCCTCGCGCGTGGACGGGTCCAAGTGTAAGTGTTCCCGGAAGGGGCCCAAGATCCGCTAC 310

Qy         311 AGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGAGAAGATGGTT 370

Db         311 AGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCACACTGCGAGGAGAAGATGGTT 370

Qy         371 ATCATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCTGCACCCCAAG 430

Db         371 ATCGTCACCACCAAGAGCATGTCCAGGTACCGGGGCCAGGAGCACTGCCTGCACCCTAAG 430

Qy         431 CTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAAGCGCAGGGTC 490

Db         431 CTGCAGAGCACCAAACGCTTCATCAAGTGGTACAATGCCTGGAACGAGAAGCGCAGGGTC 490

Qy         491 TACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTGGGAGACTTGT 550

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Qy         551 GCAAAGGACTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 610

Db         551 GCAGAGGACTTTGCAGATT----------------------------------AAAATAA 576

Qy         611 AAAGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGAAGCACTTTTT 670

Db         577 AAGCCCTTTCTTTCTCACAAGCATAAG--ACAAATTATATATTGCTATGAAGCTCTTCTT 634

Qy         671 ACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGATGGGAGACCC 730

Db         635 ACC-AGGGTCAGTTTTTACATTTTATAGCTGTGTGTGAAAGGCTTCCAGATGTGAGATCC 693

Qy         731 ATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTT 770

Db         694 AGCTCGCCTGCGCACCAGACTTCATTACAAGTGGCTTTTT 733
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RESULT 8
US-09-724-864-66
; Sequence 66, Application US/09724864
; Patent No. 6380362
; GENERAL INFORMATION:
; APPLICANT: Watson, James D
; APPLICANT: Murison, James G.
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed
; TITLE OF INVENTION: by the polynucleotides and methods for their use.
; FILE REFERENCE: 11000.1050U1
; CURRENT APPLICATION NUMBER: US/09/724,864
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 66
;   LENGTH: 764
;   TYPE: DNA
;   ORGANISM: Mouse
US-09-724-864-66

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  Query Match              26.6%;  Score 448;  DB 4;  Length 764;
  Best Local Similarity    79.7%;  Pred. No. 7.6e-96;
  Matches  606;  Conservative    0;  Mismatches  115;  Indels   39;  Gaps    5;

Qy          11 GCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGGCGCAGCCGGA 70

Db          13 GCCAAGCGCACCAGGCACCGCGACAGAC-GGCAGGAGCACCCATCGACGGGCGTACTGGA 71

Qy          71 GCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCTGGGTGGCGTC 130

Db          72 GCGAGCCGAGCAGAGCAGAGAGAGGCGTGCTTGAAACCGAGAACCAAGCCGGGCGGCATC 131

Qy         131 TCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCCACGCCGCGCC 190

Db         132 CCCCGGCCGCCGCACGCACAGGCCGGCGCCCTCCTTGCCTCCCTGCTCCC-CACCGCGCC 190

Qy         191 CCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCTGGCGCTGTAC 250

Db         191 CCTCCGGCCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTCCTGGCGCTGTGC 250

Qy         251 ACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAAGATCCGCTAC 310

Db         251 GCCTCGCGCGTGGACGGGTCCAAGTGTAAGTGTTCCCGGAAGGGGCCCAAGATCCGCTAC 310

Qy         311 AGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGAGAAGATGGTT 370

Db         311 AGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCACACTGCGAGGAGAAGATGGTT 370

Qy         371 ATCATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCTGCACCCCAAG 430

Db         371 ATCGTCACCACCAAGAGCATGTCCAGGTACCGGGGCCAGGAGCACTGCCTGCACCCTAAG 430

Qy         431 CTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAAGCGCAGGGTC 490

Db         431 CTGCAGAGCACCAAACGCTTCATCAAGTGGTACAATGCCTGGAACGAGAAGCGCAGGGTC 490

Qy         491 TACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTGGGAGACTTGT 550

Db         491 TACGAAGAATAGGGTGGACGATCATGGAAAGAAAAACTCCAGGCCAGTTGAGAGACTTCA 550

Qy         551 GCAAAGGACTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 610

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Qy         611 AAAGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGAAGCACTTTTT 670

Db         577 AAGCCCTTTCTTTCTCACAAGCATAAG--ACAAATTATATATTGCTATGAAGCTCTTCTT 634

Qy         671 ACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGATGGGAGACCC 730

Db         635 ACC-AGGGTCAGTTTTTACATTTTATAGCTGTGTGTGAAAGGCTTCCAGATGTGAGATCC 693

Qy         731 ATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTT 770

Db         694 AGCTCGCCTGCGCACCAGACTTCATTACAAGTGGCTTTTT 733
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RESULT 9
US-09-312-283C-263
; Sequence 263, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011c2
; CURRENT APPLICATION NUMBER: US/09/312,283C

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;  CURRENT FILING DATE:  1999-05-14
;  NUMBER OF SEQ ID NOS: 425
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 263
;   LENGTH: 764
;   TYPE: DNA
;   ORGANISM: Mouse
US-09-312-283C-263

  Query Match             26.6%;  Score 448;  DB 4;  Length 764;
  Best Local Similarity   79.7%;  Pred. No. 7.6e-96;
  Matches  606;  Conservative    0;  Mismatches  115;  Indels   39;  Gaps    5;

Qy          11 GCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGGCGCAGCCGGA 70
               ||  || || |    |||| || |||||| | |  | ||| ||| ||||||      | |||
Db          13 GCCAAGCGCACCAGGCACCGCGACAGAC-GGCAGGAGCACCCATCGACGGGCGTACTGGA 71

Qy          71 GCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCTGGGTGGCGTC 130
               || ||| |||| |    | | |    || ||      ||  | | ||| ||| ||| ||
Db          72 GCGAGCCGAGCAGAGCAGAGAGAGGCGTGCTTGAAACCGAGAACCAAGCCGGGCGGCATC 131

Qy         131 TCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCCACGCCGCGCC 190
               || |||||||| |   || |||| ||||||||     |||||||||| | |||||||
Db         132 CCCCGGCCGCCGCACGCACAGGCCGGCGCCCTCCTTGCCTCCCTGCTCCC-CACCGCGCC 190

Qy         191 CCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGGCGCTGTAC 250
               ||||||| |||||||||||||||||||||||||||||||||||||| ||||||||| |
Db         191 CCTCCGGCCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTCCTGGCGCTGTGC 250

Qy         251 ACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAAGATCCGCTAC 310
               ||  |||| |||||||||||||| || ||||| |||||||||||| ||||||||||||||
Db         251 GCCTCGCGCGTGGACGGGTCCAAGTGTAAGTGTTCCCGGAAGGGGCCCAAGATCCGCTAC 310

Qy         311 AGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGAGAAGATGGTT 370
               |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db         311 AGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCACACTGCGAGGAGAAGATGGTT 370

Qy         371 ATCATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCTGCACCCCAAG 430
               ||| |||||||||||||| |||||||||||||| || |||||||||||||||||||| |||
Db         371 ATCGTCACCACCAAGAGCATGTCCAGGTACCGGGGCCAGGAGCACTGCCTGCACCCTAAG 430

Qy         431 CTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAAGCGCAGGGTC 490
               |||||||||||||| |||||||||||||||||||| ||||||||||||||||||||||||
Db         431 CTGCAGAGCACCAAACGCTTCATCAAGTGGTACAATGCCTGGAACGAGAAGCGCAGGGTC 490

Qy         491 TACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTGGGAGACTTGT 550
               |||||||||||||||| |  |  |||| | |||||||||  |||||| |||||||
Db         491 TACGAAGAATAGGGTGGACGATCATGGAAAGAAAAACTCCAGGCCAGTTGAGAGACTTCA 550

Qy         551 GCAAAGGACTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 610
               ||| ||||||||||||||                                  |||| ||
Db         551 GCAGAGGACTTTGCAGATT----------------------------------AAAATAA 576

Qy         611 AAAGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGAAGCACTTTTT 670
               ||  |||||||||||||| |||||||  |||||||||||||| |||||||| ||| ||
Db         577 AAGCCCTTTCTTTCTCACAAGCATAAG--ACAAATTATATATTGCTATGAAGCTCTTCTT 634

Qy         671 ACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGATGGGAGACCC 730
               ||| | |||||||||||||||||||||||| ||| ||||||||||||||| |||| ||
Db         635 ACC-AGGGTCAGTTTTTACATTTTATAGCTGTGTGTGAAAGGCTTCCAGATGTGAGATCC 693

Qy         731 ATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTT 770
               | ||| | || || |||||||||| ||| |  |||||||
Db         694 AGCTCGCCTGCGCACCAGACTTCATTACAAGTGGCTTTTT 733


RESULT 10
US-08-825-556A-1
; Sequence 1, Application US/08825556A
; Patent No. 5910431
;  GENERAL INFORMATION:
;    APPLICANT:  Ni, Jian
;    APPLICANT:  Gentz, Reiner L.
;    APPLICANT:  Su, Jeffrey Y.
;    APPLICANT:  Li, Haodong
;    TITLE OF INVENTION:  Chemokine Alpha 2
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox, P.L.L.C.
;      STREET:  1100 New York Ave., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-2934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/825,556A
;      FILING DATE:  19-MAR-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/013,653
;      FILING DATE:  19-MAR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steffe, Eric K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.0850001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  461 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  both
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  43..375
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  79..375
;    FEATURE:
;      NAME/KEY:  sig_peptide
;      LOCATION:  43..126
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  127..375
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;      NAME/KEY:  sig_peptide
;      LOCATION:  79..126
US-08-825-556A-1

  Query Match             25.9%;  Score 435.6;  DB 2;  Length 461;
  Best Local Similarity   98.7%;  Pred. No. 4.9e-93;
  Matches  450;  Conservative    0;  Mismatches    4;  Indels    2;  Gaps    1;

Qy         130 CTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCCACGCCGCGC 189
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           6 CTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCCACGCCGCGC 65

Qy         190 CCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCTGGCGCTGTA 249
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          66 CCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCTGGCGCTGTA 125

Qy         250 CACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAAGATCCGCTA 309
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         126 CACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAAGATCCGCTA 185

Qy         310 CAGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGAGAAGATGGT 369
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         186 CAGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGAGAAGATGGT 245
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Qy        370 TATCATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCTGCACCCCAA 429
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 TATCATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCTGCACCCCAA 305

Qy        430 GCTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAAGCGCAGGGT 489
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        306 GCTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAAGCGCAGGTT 365

Qy        490 CTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTGGGAGACTTG 549
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 CTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTGGGAGACTTG 425

Qy        550 TG--CAAAGGACTTTGCAGATTAAAAAAAAAAAAAA 583
              ||  || | ||||||||||||||||||||||||||||
Db        426 TGGCAAAGGAACTTTGCAGATTAAAAAAAAAAAAAA 461
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RESULT 11
US-09-238-184-1
; Sequence 1, Application US/09238184
; Patent No. 6479633
;  GENERAL INFORMATION:
;    APPLICANT:  Ni, Jian
;    APPLICANT:  Gentz, Reiner L.
;    APPLICANT:  Su, Jeffrey Y.
;    APPLICANT:  Li, Haodong
;    TITLE OF INVENTION:  Chemokine Alpha 2
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox, P.L.L.C.
;      STREET:  1100 New York Ave., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-2934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/238,184
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/825,556
;      FILING DATE:  19-MAR-1997
;      APPLICATION NUMBER:  US 60/013,653
;      FILING DATE:  19-MAR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steffe, Eric K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.0850001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  461 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  both
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  43..375
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  79..375
;    FEATURE:
;      NAME/KEY:  sig_peptide
;      LOCATION:  43..126
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  127..375
;    FEATURE:
;      NAME/KEY:  sig_peptide
;      LOCATION:  79..126
US-09-238-184-1

  Query Match             25.9%;  Score 435.6;  DB 4;  Length 461;
  Best Local Similarity   98.7%;  Pred. No. 4.9e-93;
  Matches  450;  Conservative    0;  Mismatches    4;  Indels    2;  Gaps    1;

Qy        130 CTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCCACGCCGCGC 189
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 CTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCCACGCCGCGC 65

Qy        190 CCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCTGGCGCTGTA 249
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 CCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCTGGCGCTGTA 125

Qy        250 CACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAAGATCCGCTA 309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 CACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAAGATCCGCTA 185

Qy        310 CAGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGAGAAGATGGT 369
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CAGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGAGAAGATGGT 245

Qy        370 TATCATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCTGCACCCCAA 429
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 TATCATCACCACCAAGAGCGTGTCCAGGTACCGAGGTCAGGAGCACTGCCTGCACCCCAA 305

Qy        430 GCTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAAGCGCAGGGT 489
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        306 GCTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAAGCGCAGGTT 365

Qy        490 CTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTGGGAGACTTG 549
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 CTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTGGGAGACTTG 425

Qy        550 TG--CAAAGGACTTTGCAGATTAAAAAAAAAAAAAA 583
              ||  || | ||||||||||||||||||||||||||||
Db        426 TGGCAAAGGAACTTTGCAGATTAAAAAAAAAAAAAA 461
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RESULT 12
US-09-188-930-38
; Sequence 38, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
;  APPLICANT: Watson, James D.
;  APPLICANT: Strachan, Lorna
;  APPLICANT: Sleeman, Matthew
;  APPLICANT: Onrust, Rene
;  APPLICANT: Murison, James Greg
;  TITLE OF INVENTION: Compositions Isolated From Skin Cells
;  TITLE OF INVENTION: and Methods For Their Use
;  FILE REFERENCE: 11000.1011c1
;  CURRENT APPLICATION NUMBER: US/09/188,930A
;  CURRENT FILING DATE: 1998-11-09
;  NUMBER OF SEQ ID NOS: 348
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 38
;   LENGTH: 766
;   TYPE: DNA
;   ORGANISM: mouse
US-09-188-930-38

  Query Match             25.3%;  Score 426;  DB 3;  Length 766;
  Best Local Similarity   79.5%;  Pred. No. 1.1e-90;
  Matches  606;  Conservative    0;  Mismatches  115;  Indels   41;  Gaps    7;

Qy         11 GCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGGCGCAGCCGGA 70
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Db         13 GCCAAGCGCACCAGGCACCGCGACAGAC-GGCAGGAGCACCCATCGACGGGCGTACTGGA 71

Qy         71 GCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCTGGGTGGCGTC 130

Db         72 GCGAGCCGAGCAGAGCAGAGAGAGGCGTGCTTGAAACCGAGAACCAAGCCGGGCGGCATC 131

Qy        131 TCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCCACGCCGCGCC 190

Db        132 CCCCGGCCGCCGCACGCACAGGCCGGCGCCCTCCTTGCCTCCCTGCTCCC-CACCGCGCC 190

Qy        191 CCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCTGGCGCTGTAC 250

Db        191 CCTCCGGCCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTCCTGGCGCTGTGC 250

Qy        251 ACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAAGATCCGCTAC 310

Db        251 GCCTCGCGCGTGGACGGGTCCAAGTGTAAGTGTTCCCGGAAGGGGCCCAAGATCCGCTAC 310

Qy        311 AGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGAGAAGATGGTT 370

Db        311 AGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCACACTGCGAGGAGAAGATGGTT 370

Qy        371 ATCATCACCACC-AAGAGCGTGTCC-AGGTACCGAGGTCAGGAGCACTGCCTGCACCCCA 428

Db        371 ATCGTCACCACCAAAGAGCATGTCCAAGGTACCGGGGCCAGGAGCACTGCCTGCACCCTA 430

Qy        429 AGCTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAAGCGCAGGG 488

Db        431 AGCTGCAGAGCACCAAACGCTTCATCAAGTGGTACAATGCCTGGAACGAGAAGCGCAGGG 490

Qy        489 TCTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTGGGAGACTT 548

Db        491 TCTACGAAGAATAGGGTGGACGATCATGGAAAGAAAAACTCCAGGCCAGTTGAGAGACTT 550

Qy        549 GTGCAAAGGACTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 608

Db        551 CAGCAGAGGACTTTGCAGATT----------------------------------AAAAT 576

Qy        609 AAAAAGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGAAGCACTTT 668

Db        577 AAAAGCCCTTTCTTTCTCACAAGCATAAG--ACAAATTATATATTGCTATGAAGCTCTTC 634

Qy        669 TTACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGATGGGAGAC 728

Db        635 TTACC-AGGGTCAGTTTTTACATTTTATAGCTGTGTGTGAAAGGCTTCCAGATGTGAGAT 693

Qy        729 CCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTT 770

Db        694 CCAGCTCGCCTGCGCACCAGACTTCATTACAAGTGGCTTTTT 735
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RESULT 13
US-09-312-283C-38
; Sequence 38, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011c2
; CURRENT APPLICATION NUMBER: US/09/312,283C
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 766
; TYPE: DNA

; ORGANISM: Mouse
US-09-312-283C-38

Query Match 25.3%; Score 426; DB 4; Length 766;
Best Local Similarity 79.5%; Pred. No. 1.1e-90;
Matches 606; Conservative 0; Mismatches 115; Indels 41; Gaps 7;

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Qy         11 GCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGGCGCAGCCGGA 70

Db         13 GCCAAGCGCACCAGGCACCGCGACAGAC-GGCAGGAGCACCCATCGACGGGCGTACTGGA 71

Qy         71 GCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCTGGGTGGCGTC 130

Db         72 GCGAGCCGAGCAGAGCAGAGAGAGGCGTGCTTGAAACCGAGAACCAAGCCGGGCGGCATC 131

Qy        131 TCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCCACGCCGCGCC 190

Db        132 CCCCGGCCGCCGCACGCACAGGCCGGCGCCCTCCTTGCCTCCCTGCTCCC-CACCGCGCC 190

Qy        191 CCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCTGGCGCTGTAC 250

Db        191 CCTCCGGCCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTCCTGGCGCTGTGC 250

Qy        251 ACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAAGATCCGCTAC 310

Db        251 GCCTCGCGCGTGGACGGGTCCAAGTGTAAGTGTTCCCGGAAGGGGCCCAAGATCCGCTAC 310

Qy        311 AGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGAGAAGATGGTT 370

Db        311 AGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCACACTGCGAGGAGAAGATGGTT 370

Qy        371 ATCATCACCACC-AAGAGCGTGTCC-AGGTACCGAGGTCAGGAGCACTGCCTGCACCCCA 428

Db        371 ATCGTCACCACCAAAGAGCATGTCCAAGGTACCGGGGCCAGGAGCACTGCCTGCACCCTA 430

Qy        429 AGCTGCAGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAAGCGCAGGG 488

Db        431 AGCTGCAGAGCACCAAACGCTTCATCAAGTGGTACAATGCCTGGAACGAGAAGCGCAGGG 490

Qy        489 TCTACGAAGAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTGGGAGACTT 548

Db        491 TCTACGAAGAATAGGGTGGACGATCATGGAAAGAAAAACTCCAGGCCAGTTGAGAGACTT 550

Qy        549 GTGCAAAGGACTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 608

Db        551 CAGCAGAGGACTTTGCAGATT----------------------------------AAAAT 576

Qy        609 AAAAAGCCTTTCTTTCTCACAGGCATAAGACACAAATTATATATTGTTATGAAGCACTTT 668

Db        577 AAAAGCCCTTTCTTTCTCACAAGCATAAG--ACAAATTATATATTGCTATGAAGCTCTTC 634

Qy        669 TTACCAACGGTCAGTTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGATGGGAGAC 728

Db        635 TTACC-AGGGTCAGTTTTTACATTTTATAGCTGTGTGTGAAAGGCTTCCAGATGTGAGAT 693

Qy        729 CCATCTCTCTTGTGCTCCAGACTTCATCACAGGCTGCTTTTT 770

Db        694 CCAGCTCGCCTGCGCACCAGACTTCATTACAAGTGGCTTTTT 735
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RESULT 14
US-09-673-395A-59/c
; Sequence 59, Application US/09673395A
; Patent No. 6620923
; GENERAL INFORMATION:
; APPLICANT: SPECHT, THOMAS
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHMITT, ARMIN
; APPLICANT: PILARSKY, CHRISTIAN
; APPLICANT: DAHL, EDGAR
; APPLICANT: ROSENTHAL, ANDRE
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE
; FILE REFERENCE: ALBRE-12

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;  CURRENT APPLICATION NUMBER: US/09/673,395A
;  CURRENT FILING DATE:  2000-10-17
;  NUMBER OF SEQ ID NOS: 637
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
;   LENGTH: 1630
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-673-395A-59

  Query Match             20.9%;  Score 352.8;  DB 4;  Length 1630;
  Best Local Similarity   90.8%;  Pred. No. 2.5e-73;
  Matches  432;  Conservative    0;  Mismatches   37;  Indels    7;  Gaps    5;

Qy        782 GAAAACTCATGCCTTTCCTTTTTAAAAAATGCTTTTTTGTATTTGTCCATACGTCACTAT 841
              ||||      |   |||  |||||       |  ||||||||||||||||||||||||||
Db        577 GAAAGGCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGTATTTGTCCATACGTCACTAT 518

Qy        842 ACATCTGAGCTTTATAAGCGCCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTGC 901
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        517 ACATCTGAGCTTTATAAGCACCCGGGAGGAACAATGAGCTTGGTGGACACATTTCATTGC 458

Qy        902 AGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCACA 961
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        457 AGTGTTGCTCCATTCCTAGCTTGGGAAGCTTCCGCTTAGAGGTCCTGGCGCCTCGGCACA 398

Qy        962 GCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTGG 1021
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        397 GCTGCCACGGGCTCTCCTGGGCTTATGGCCGGTCACAGCCTCAGTGTGACTCCACAGTGG 338

Qy       1022 CCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAAG 1081
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        337 CCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCTCTGCATCTGTTCTCTGAGGAACTCAAG 278

Qy       1082 TTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCT-GGTTAATTTTTACACACCCTA-GG 1139
              |||||||||||||||||||||||||||||||||| |||||||||||||||||||| || 
Db        277 TTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCCTGGGTTAATTTTTACACACCCTAGGG 218

Qy       1140 AAACATTTCCAAGATCCTGTGAT-GGCGAGACAAATGATCCTTAAAGAAGG---TGTGGG 1195
              |||||||||||||||||||||| |||||||||||||||||||  | |   || |||
Db        217 AAACATTTCCAAGATCCTGTGATGGGCGAGACAAATGATCCTTAAAAGAAGGTTTGGGGG 158

Qy       1196 GTCTTTCCCAACCTGA-GGATTTCTGAAAGGTTCACAGGTTCAATATTTAATGCTT 1250
                ||||||||||||| || ||| |||||||||||||||||  | | | |  ||
Db        157 TCTTTTCCCAACCTGAGGGTTTTTTGAAAGGTTCACAGGTTTCAAGTATTTTAATT 102


RESULT 15
US-09-188-930-270
; Sequence 270, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
;  APPLICANT: Watson, James D.
;  APPLICANT: Strachan, Lorna
;  APPLICANT: Sleeman, Matthew
;  APPLICANT: Onrust, Rene
;  APPLICANT: Murison, James Greg
;  TITLE OF INVENTION: Compositions Isolated From Skin Cells
;  TITLE OF INVENTION: and Methods For Their Use
;  FILE REFERENCE: 11000.1011c1
;  CURRENT APPLICATION NUMBER: US/09/188,930A
;  CURRENT FILING DATE: 1998-11-09
;  NUMBER OF SEQ ID NOS: 348
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 270
;   LENGTH: 288
;   TYPE: DNA
;   ORGANISM: Mouse
US-09-188-930-270

  Query Match             17.1%;  Score 288;  DB 3;  Length 288;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-58;
  Matches  288;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        215 GCGGCCGCGCTGCTCCTGCTGCTGCTGGCGCTGTACACCGCGCGTGTGGACGGGTCCAAA 274
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCGGCCGCGCTGCTCCTGCTGCTGCTGGCGCTGTACACCGCGCGTGTGGACGGGTCCAAA 60

Qy        275 TGCAAGTGCTCCCGGAAGGGACCCAAGATCCGCTACAGCGACGTGAAGAAGCTGGAAATG 334
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGCAAGTGCTCCCGGAAGGGACCCAAGATCCGCTACAGCGACGTGAAGAAGCTGGAAATG 120

Qy        335 AAGCCAAAGTACCCGCACTGCGAGGAGAAGATGGTTATCATCACCACCAAGAGCGTGTCC 394
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAGCCAAAGTACCCGCACTGCGAGGAGAAGATGGTTATCATCACCACCAAGAGCGTGTCC 180

Qy        395 AGGTACCGAGGTCAGGAGCACTGCCTGCACCCCAAGCTGCAGAGCACCAAGCGCTTCATC 454
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGGTACCGAGGTCAGGAGCACTGCCTGCACCCCAAGCTGCAGAGCACCAAGCGCTTCATC 240

Qy        455 AAGTGGTACAACGCCTGGAACGAGAAGCGCAGGGTCTACGAAGAATAG 502
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAGTGGTACAACGCCTGGAACGAGAAGCGCAGGGTCTACGAAGAATAG 288


Search completed: April 26, 2004, 10:29:53
Job time : 141 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 22, 2004, 12:26:32 ; Search time 17 Seconds
(without alignments)
339.987 Million cell updates/sec

Title: US-09-978-189-370
Perfect score: 587
Sequence: 1 MSLLPRRAPPVSMRLLAAAL.....TKRFIKWYNAWNEKRRVYEE 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	527	89.8	99	1	SZ14_HUMAN	O95715 homo sapien
2	489	83.3	99	1	SZ14_MOUSE	Q9wuq5 mus musculu
3	143.5	24.4	100	1	MI2B_RAT	Q10747 rattus norv
4	138	23.5	100	1	MIP2_MOUSE	P10889 mus musculu
5	131	22.3	101	1	GRO_CRIGR	P09340 cricetulus
6	128.5	21.9	107	1	MI2A_HUMAN	P19875 homo sapien
7	127.5	21.7	103	1	GRO_SHEEP	O46678 ovis aries
8	124	21.1	100	1	MIP2_RAT	P30348 rattus norv
9	122.5	20.9	98	1	GROG_BOVIN	O46675 bos taurus
10	118.5	20.2	104	1	GRO2_RABIT	P47854 oryctolagus
11	117.5	20.0	104	1	GROB_BOVIN	O46677 bos taurus
12	117.5	20.0	107	1	GRO_HUMAN	P09341 homo sapien
13	116.5	19.8	107	1	MI2B_HUMAN	P19876 homo sapien
14	113.5	19.3	104	1	GROA_BOVIN	O46676 bos taurus
15	111	18.9	96	1	GRO_MOUSE	P12850 mus musculu
16	104.5	17.8	68	1	MI2A_RAT	Q10746 rattus norv
17	103	17.5	104	1	GRO_CAVPO	O55235 cavia porce
18	103	17.5	117	1	AMC2_PIG	P22952 sus scrofa
19	97	16.5	96	1	GRO_RAT	P14095 rattus norv
20	94.5	16.1	126	1	SZ09_MOUSE	P18340 mus musculu
21	90.5	15.4	71	1	GRO1_RABIT	P30782 oryctolagus
22	87.5	14.9	125	1	SZ09_HUMAN	Q07325 homo sapien
23	87	14.8	114	1	SZ06_HUMAN	P80162 homo sapien
24	86	14.7	112	1	SZ06_BOVIN	P80221 bos taurus
25	84	14.3	94	1	SZ11_HUMAN	O14625 homo sapien
26	84	14.3	104	1	PF4V_HUMAN	P10720 homo sapien
27	83.5	14.2	101	1	IL8_CANFA	P41324 canis famil
28	83.5	14.2	101	1	IL8_FELCA	Q9xsx5 felis silve
29	82.5	14.1	103	1	IL8_PIG	P26894 sus scrofa
30	82.5	14.1	128	1	SZ07_HUMAN	P02775 h platelet
31	82	14.0	94	1	SY26_HUMAN	Q9y258 homo sapien
32	82	14.0	130	1	SZ05_RAT	P97885 rattus norv
33	81.5	13.9	98	1	SZ10_HUMAN	P02778 homo sapien
34	81	13.8	101	1	PLF4_HUMAN	P02776 homo sapien
35	80.5	13.7	98	1	SZ10_MOUSE	P17515 mus musculu
36	80.5	13.7	101	1	IL8_BOVIN	P79255 bos taurus
37	80.5	13.7	103	1	EMF1_CHICK	P08317 gallus gall
38	80	13.6	119	1	SZ07_PIG	P43030 sus scrofa
39	79.5	13.5	101	1	IL8_SHEEP	P36925 ovis aries
40	76.5	13.0	114	1	SZ05_HUMAN	P42830 homo sapien
41	76	12.9	132	1	SZ05_MOUSE	P50228 mus musculu
42	75.5	12.9	97	1	IL8_HORSE	O62812 equus cabal
43	73	12.4	89	1	SY18_HUMAN	P55774 h small ind
44	73	12.4	105	1	PLF4_RAT	P06765 rattus norv
45	72.5	12.4	101	1	IL8_RABIT	P19874 oryctolagus

ALIGNMENTS

RESULT 1
SZ14_HUMAN
ID SZ14_HUMAN STANDARD; PRT; 99 AA.
AC O95715; Q86U69; Q9BTR1;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Small inducible cytokine B14 precursor (CXCL14) (Chemokine BRAK).
GN CXCL14 OR SCYB14 OR NJAC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99160416; PubMed=10049774;
RA Hromas R., Broxmeyer H.E., Kim C., Nakshatri H., Christopherson K. II,
RA Azam M., Hou Y.-H.;
RT "Cloning of BRAK, a novel divergent CXC chemokine preferentially
RT expressed in normal versus malignant cells.";
RL Biochem. Biophys. Res. Commun. 255:703-706(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Oral epithelium;
RA Frederick M.F., Henderson Y., Xu X., El-Naggar A.K., Wu H.,
RA Hudson J.M., Clayman G.L.;
RT "Identification of a novel chemokine family member with altered
RT expression in human head and neck squamous cell carcinoma.";
RL Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length CDSs in BD Creator(TM) system donor
RT vector.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

```
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Not chemotactive for T-cells, B-cells, monocytes,
CC       natural killer cells or ghranulocytes. Does not inhibit
CC       proliferation of myeloid progenitors in colony formation assays.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Expressed in heart, brain, placenta, lung,
CC       liver, skeletal muscle, kidney and pancreas. Highly expressed in
CC       normal tissue without inflammatory stimuli and infrequently
CC       expressed in cancer cell lines.
CC   -!- SIMILARITY: Belongs to the intercrine alpha (chemokine CxC)
CC       family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF073957; AAD03839.1; -.
DR   EMBL; AF144103; AAD38944.1; -.
DR   EMBL; BT007080; AAP35743.1; ALT_INIT.
DR   EMBL; BC003513; AAH03513.1; ALT_INIT.
DR   Genew; HGNC:10640; CXCL14.
DR   MIM; 604186; -.
DR   GO; GO:0008009; F:chemokine activity; TAS.
DR   GO; GO:0007267; P:cell-cell signaling; TAS.
DR   GO; GO:0006935; P:chemotaxis; TAS.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   InterPro; IPR001089; CXC_chmkine_sml1.
DR   Pfam; PF00048; IL8; 1.
DR   PROSITE; PS00471; SMALL_CYTOKINES_CXC; FALSE_NEG.
KW   Cytokine; Signal.
FT   SIGNAL        1     22       POTENTIAL.
FT   CHAIN        23     99       SMALL INDUCIBLE CYTOKINE B14.
FT   DISULFID     25     51       BY SIMILARITY.
FT   DISULFID     27     72       BY SIMILARITY.
SQ   SEQUENCE   99 AA;  11772 MW;  998802D8FC659C1D CRC64;

  Query Match             89.8%;  Score 527;  DB 1;  Length 99;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-50;
  Matches   99;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 MRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIITT 72
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIITT 60

Qy         73 KSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
              |||||||||||||||||||||||||||||||||||||||
Db         61 KSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 99


RESULT 2
SZ14_MOUSE
ID   SZ14_MOUSE     STANDARD;      PRT;    99 AA.
AC   Q9WUQ5;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Small inducible cytokine B14 precursor (CXCL14) (Chemokine BRAK)
DE   (Kidney-expressed chemokine CXC).
GN   CXCL14 OR SCYB14 OR KEC.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99160416; PubMed=10049774;
RA   Hromas R., Broxmeyer H.E., Kim C., Nakshatri H., Christopherson K. II,
RA   Azam M., Hou Y.-H.;
RT   "Cloning of BRAK, a novel divergent CXC chemokine preferentially
RT   expressed in normal versus malignant cells.";
RL   Biochem. Biophys. Res. Commun. 255:703-706(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C3H;
RA   Wang L., Deng L., Raikwar N., Sahota A., Tischfield J.A.;
RT   "Identification of a kidney-expressed chemokine (KEC), a member of the
RT   CXC family, that is selectively elevated in aprt knockout mice.";
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC   -!- SIMILARITY: Belongs to the intercrine alpha (chemokine CxC)
CC       family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF152377; AAD34157.1; -.
DR   EMBL; AF192557; AAF03753.1; -.
DR   MGD; MGI:1888514; Cxcl14.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   InterPro; IPR001089; CXC_chmkine_sml1.
DR   Pfam; PF00048; IL8; 1.
DR   PROSITE; PS00471; SMALL_CYTOKINES_CXC; FALSE_NEG.
KW   Cytokine; Signal.
FT   SIGNAL        1     22       POTENTIAL.
FT   CHAIN        23     99       SMALL INDUCIBLE CYTOKINE B14.
FT   DISULFID     25     51       BY SIMILARITY.
FT   DISULFID     27     72       BY SIMILARITY.
FT   CONFLICT     64     64       F -> S (IN REF. 2).
SQ   SEQUENCE   99 AA;  11802 MW;  754BD6CDA01CA25D CRC64;

  Query Match             83.3%;  Score 489;  DB 1;  Length 99;
  Best Local Similarity   91.9%;  Pred. No. 2.2e-46;
  Matches   91;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy         13 MRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIITT 72
              ||||||||||||||||    :|||||||||||||||||||||||||||||||||||:||
Db          1 MRLLAAALLLLLLALCVRALDGSKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIVTT 60

Qy         73 KSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
              ||: |||||||||||||||||||||||||||||||||||
Db         61 KSMFRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 99


RESULT 3
MI2B_RAT
ID   MI2B_RAT       STANDARD;      PRT;   100 AA.
AC   Q10747;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Macrophage inflammatory protein-2-beta precursor (MIP2-beta) (CINC-
DE   2-beta).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 33-100.
RC   STRAIN=Wistar;
RX   MEDLINE=94318061; PubMed=8043001;
RA   Nakagawa H., Komorita N., Shibata F., Ikesue A., Konishi K.,
RA   Fujioka M., Kato H.;
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RT   "Identification of cytokine-induced neutrophil chemoattractants
RT   (CINC), rat GRO/CINC-2 alpha and CINC-2 beta, produced by granulation
RT   tissue in culture: purification, complete amino acid sequences and
RT   characterization.";
RL   Biochem. J. 301:545-550(1994).
RN   [2]
RP   SEQUENCE OF 33-52.
RC   STRAIN=Wistar;
RX   MEDLINE=96183056; PubMed=8607872;
RA   Nakagawa H., Shiota S., Takano K., Shibata F., Kato H.;
RT   "Cytokine-induced neutrophil chemoattractant (CINC)-2 alpha, a novel
RT   member of rat GRO/CINCs, is a predominant chemokine produced by
RT   lipopolysaccharide-stimulated rat macrophages in culture.";
RL   Biochem. Biophys. Res. Commun. 220:945-948(1996).
CC   -!- FUNCTION: May play a role in inflammation and exert its effects
CC       on endothelial cells in an autocrine fashion.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the intercrine alpha (chemokine CxC)
CC       family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; D21095; BAA04657.1; -.
DR   PIR; S46198; S46198.
DR   HSSP; P10889; 1MI2.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   InterPro; IPR001089; CXC_chmkine_sml1.
DR   Pfam; PF00048; IL8; 1.
DR   SMART; SM00199; SCY; 1.
DR   PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
KW   Cytokine; Chemotaxis; Inflammatory response; Signal.
FT   SIGNAL        1     32
FT   CHAIN        33    100       MACROPHAGE INFLAMMATORY PROTEIN-
FT                                 2-BETA.
FT   DISULFID     37     63       BY SIMILARITY.
FT   DISULFID     39     79       BY SIMILARITY.
SQ   SEQUENCE   100 AA;  10989 MW;  EB53ECEFE30909D2 CRC64;

  Query Match             24.4%;  Score 143.5;  DB 1;  Length 100;
  Best Local Similarity   35.1%;  Pred. No. 9e-09;
  Matches   34;  Conservative   19;  Mismatches   31;  Indels   13;  Gaps    3;

Qy          8 APPVSMRLLAAALLLLLLALYTARVDGS-------KCKCSRKGPKIRYSDVKKLEMKPKY 60
              ||| : ||| |||||||| : |:            :|:| :  |:: : ::: | : |
Db          2 APP-TRRLLNAALLLLLLLMATSHQPSGTVVARELRCQCLKTLPRVDFENIQSLTVTPPG 60

Qy         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIK 97
              ||| :  || | |      ||| ||:|:    :: |:
Db         61 PHCTQTEVIATLKD-----GQEVCLNPQAPRLQKIIQ 92


RESULT 4
MIP2_MOUSE
ID   MIP2_MOUSE     STANDARD;      PRT;   100 AA.
AC   P10889;
DT   01-JUL-1989 (Rel. 11, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Macrophage inflammatory protein 2 precursor (MIP2).
GN   CXCL2 OR SCYB2 OR MIP2 OR MIP-2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90354792; PubMed=2201751;
RA   Tekamp-Olson P., Gallegos C., Bauer D., McClain J., Sherry B.,
RA   Fabre M., van Deventer S., Cerami A.;
RT   "Cloning and characterization of cDNAs for murine macrophage
RT   inflammatory protein 2 and its human homologues.";
RL   J. Exp. Med. 172:911-919(1990).
RN   [2]
RP   SEQUENCE OF 28-59.
RX   MEDLINE=89098980; PubMed=2643119;
RA   Wolpe S.D., Sherry B., Juers D., Davatelis G., Yurt R.W., Cerami A.;
RT   "Identification and characterization of macrophage inflammatory
RT   protein 2.";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:612-616(1989).
RN   [3]
RP   STRUCTURE BY NMR.
RX   MEDLINE=98285558; PubMed=9622482;
RA   Shao W., Jerva L.F., West J., Lolis E., Schweitzer B.I.;
RT   "Solution structure of murine macrophage inflammatory protein-2.";
RL   Biochemistry 37:8303-8313(1998).
CC   -!- FUNCTION: Chemotactic for human polymorphonuclear leukocytes but
CC       does not induce chemokinesis or an oxidative burst.
CC   -!- SUBUNIT: Homotetramer.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the intercrine alpha (chemokine CxC)
CC       family.
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X53798; CAA37807.1; -.
DR   PIR; JH0200; JH0200.
DR   PDB; 1MI2; 29-APR-98.
DR   MGD; MGI:1340094; Cxcl2.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   InterPro; IPR001089; CXC_chmkine_sml1.
DR   Pfam; PF00048; IL8; 1.
DR   PRINTS; PR00437; SMALLCYTKCXC.
DR   SMART; SM00199; SCY; 1.
DR   PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
KW   Cytokine; Chemotaxis; Inflammatory response; Signal; 3D-structure.
FT   SIGNAL        1     27
FT   CHAIN        28    100       MACROPHAGE INFLAMMATORY PROTEIN 2.
FT   DISULFID     36     62
FT   DISULFID     38     78
FT   STRAND       42     42
FT   TURN         45     46
FT   HELIX        47     49
FT   STRAND       52     56
FT   TURN         60     62
FT   STRAND       66     71
FT   TURN         72     74
FT   STRAND       75     79
FT   TURN         85     86
FT   HELIX        87     94
FT   TURN         96     97
SQ   SEQUENCE   100 AA;  10621 MW;  B9EF0A3218EE92B5 CRC64;

  Query Match             23.5%;  Score 138;  DB 1;  Length 100;
  Best Local Similarity   33.3%;  Pred. No. 3.6e-08;
  Matches   32;  Conservative   21;  Mismatches   31;  Indels   12;  Gaps    3;

Qy          8 APPVSMRLLAAALLLLLLALYTARVDGS------KCKCSRKGPKIRYSDVKKLEMKPKYP 61
              ||| : |||:|||:||||      :  |:      :|:| :  |:: : ::: | : |  |
Db          2 APP-TCRLLSAALVLLLLLATNHQATGAVVASELRCQCLKTLPRVDFKNIQSLSVTPPGP 60

Qy         62 HCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIK 97
              || :  || | |      ||: || |:    :: |:
Db         61 HCAQTEVIATLKG-----GQKVCLDPEAPLVQKIIQ 91
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RESULT 5
GRO_CRIGR
ID   GRO_CRIGR      STANDARD;      PRT;   101 AA.
AC   P09340;
DT   01-MAR-1989 (Rel. 10, Created)
DT   01-MAR-1989 (Rel. 10, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Growth regulated protein precursor (CXCL1).
GN   CXCL1 OR SCYB1 OR GRO.
OS   Cricetulus griseus (Chinese hamster).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC   Cricetulus.
OX   NCBI_TaxID=10029;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88041072; PubMed=2890161;
RA   Anisowicz A., Bardwell L., Sager R.;
RT   "Constitutive overexpression of a growth-regulated gene in
RT   transformed Chinese hamster and human cells.";
RL   Proc. Natl. Acad. Sci. U.S.A. 84:7188-7192(1987).
CC   -!- FUNCTION: Has chemotactic activity for neutrophils.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the intercrine alpha (chemokine CxC)
CC       family.
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CC   ---------------------------------------------------------------------
DR   EMBL; J03560; AAA36985.1; -.
DR   PIR; B28414; B28414.
DR   HSSP; P19875; 1QNK.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   InterPro; IPR001089; CXC_chmkine_sm11.
DR   Pfam; PF00048; IL8; 1.
DR   PRINTS; PR00437; SMALLCYTKCXC.
DR   SMART; SM00199; SCY; 1.
DR   PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
KW   Cytokine; Growth factor; Inflammatory response; Signal.
FT   SIGNAL        1     28       POTENTIAL.
FT   CHAIN        29    101       GROWTH REGULATED PROTEIN.
FT   DISULFID     37     63       BY SIMILARITY.
FT   DISULFID     39     79       BY SIMILARITY.
SQ   SEQUENCE   101 AA;  10893 MW;  666FB7E9CC512019 CRC64;

  Query Match             22.3%;  Score 131;  DB 1;  Length 101;
  Best Local Similarity   31.6%;  Pred. No. 2.1e-07;
  Matches   30;  Conservative   21;  Mismatches   32;  Indels   12;  Gaps    2;

Qy         10 PVSMRLLAAALLLLLLALYTARV-------DGSKCKCSRKGPKIRYSDVKKLEMKPKYPH 62
              |  :  || | ||||| | |:|:       :  :|:| :    :   ::: |:: |  ||
Db          3 PATRSLLRAPLLLLLLLATSRLATGAPVANELRCQCLQTMTGVHLKNIQSLKVTPPGPH 62

Qy         63 CEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIK 97
              | :  || | |:     ||| ||:|:     :: ::
Db         63 CTQTEVIATLKN-----GQEACLNPEAPMVQKIVQ 92


RESULT 6
MI2A_HUMAN
ID   MI2A_HUMAN     STANDARD;      PRT;   107 AA.
AC   P19875; Q9UPB8;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Macrophage inflammatory protein-2-alpha precursor (MIP2-alpha) (CXCL2)
DE   (Growth regulated protein beta) (Gro-beta).
GN   CXCL2 OR GRO2 OR SCYB2 OR GROB OR MIP2A.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Histiocytic lymphoma;
RX   MEDLINE=90354792; PubMed=2201751;
RA   Tekamp-Olson P., Gallegos C., Bauer D., McClain J., Sherry B.,
RA   Fabre M., van Deventer S., Cerami A.;
RT   "Cloning and characterization of cDNAs for murine macrophage
RT   inflammatory protein 2 and its human homologues.";
RL   J. Exp. Med. 172:911-919(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90377259; PubMed=2078213;
RA   Iida N., Grotendorst G.R.;
RT   "Cloning and sequencing of a new gro transcript from activated human
RT   monocytes: expression in leukocytes and wound tissue.";
RL   Mol. Cell. Biol. 10:5596-5599(1990).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91017578; PubMed=2217207;
RA   Haskill S., Peace A., Morris J., Sporn S.A., Anisowicz A., Lee S.W.,
RA   Smith T., Martin G., Ralph P., Sager R.;
RT   "Identification of three related human GRO genes encoding cytokine
RT   functions.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:7732-7736(1990).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Eye;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [5]
RP   SEQUENCE OF 35-107 FROM N.A.
RA   Jang J.S., Kim B.E.;
RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   STRUCTURE BY NMR OF 39-107.
RX   MEDLINE=20069929; PubMed=10600366;
RA   Qian Y.Q., Johanson K.O., McDevitt P.;
RT   "Nuclear magnetic resonance solution structure of truncated human
RT   GRObeta [5-73] and its structural comparison with CXC chemokine
RT   family members GROalpha and IL-8.";
RL   J. Mol. Biol. 294:1065-1072(1999).
CC   -!- FUNCTION: Produced by activated monocytes and neutrophils and
CC       expressed at sites of inflammation.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the intercrine alpha (chemokine CxC)
CC       family.
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CC   ---------------------------------------------------------------------------
DR   EMBL; X53799; CAA37808.1; -.
DR   EMBL; M36820; AAA63183.1; -.
DR   EMBL; M57731; AAA63182.1; -.
DR   EMBL; BC015753; AAH15753.1; -.
DR   EMBL; AF043340; AAC03540.1; -.
DR   PIR; JH0281; JH0281.
DR   PDB; 1QNK; 04-FEB-00.
DR   Genew; HGNC:4603; CXCL2.
DR   MIM; 139110; -.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0005625; C:soluble fraction; TAS.
DR   GO; GO:0008009; F:chemokine activity; TAS.
DR   GO; GO:0006935; P:chemotaxis; TAS.
DR   GO; GO:0006954; P:inflammatory response; TAS.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   InterPro; IPR001089; CXC_chmkine_sml1.
DR   Pfam; PF00048; IL8; 1.
DR   SMART; SM00199; SCY; 1.
DR   PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
KW   Cytokine; Chemotaxis; Inflammatory response; Signal; 3D-structure.
FT   SIGNAL       1     34
FT   CHAIN        35    107       MACROPHAGE INFLAMMATORY PROTEIN-
FT                                2-ALPHA.
FT   DISULFID     43    69
FT   DISULFID     45    85
FT   STRAND       49    49
FT   TURN         54    56
FT   STRAND       57    63
FT   STRAND       73    78
FT   TURN         79    80
FT   STRAND       83    86
FT   TURN         88    89
FT   TURN         93    95
FT   TURN         98    102
SQ   SEQUENCE   107 AA;  11389 MW;  740F277E928571BA CRC64;

  Query Match             21.9%;  Score 128.5;  DB 1;  Length 107;
  Best Local Similarity   33.3%;  Pred. No. 4.2e-07;
  Matches   32;  Conservative   18;  Mismatches   35;  Indels   11;  Gaps    2;

Qy          8 APPVSMRLLAAALLLLLLALYTARVDGS------KCKCSRKGPKIRYSDVKKLEMKPKYP 61
              | | : |||  |||||||   : |  |:        :|:| :   |   ::: :::|   |
Db          8 AAPSNPRLLRVALLLLLLVAASRRAAGAPLATELRCQCLQTLQGIHLKNIQSVKVKSPGP 67

Qy         62 HCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIK 97
              || :  || | |:     ||: ||:|     |: |:
Db         68 HCAQTEVIATLKN-----GQKACLNPASPMVKKIIE 98


RESULT 7
GRO_SHEEP
ID   GRO_SHEEP      STANDARD;      PRT;   103 AA.
AC   O46678;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Growth regulated protein precursor (CXCL1).
GN   CXCL1 OR SCYB1 OR GRO.
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99152612; PubMed=10028286;
RA   Modi W.S., Yoshimura T.;
RT   "Isolation of novel GRO genes and a phylogenetic analysis of the CXC
RT   chemokine subfamily in mammals.";
RL   Mol. Biol. Evol. 16:180-193(1999).
CC   -!- FUNCTION: Has chemotactic activity for neutrophils.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the intercrine alpha (chemokine CxC)
CC       family.
CC   ---------------------------------------------------------------------------
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CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; U95814; AAB93930.1; -.
DR   HSSP; P19875; 1QNK.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   InterPro; IPR001089; CXC_chmkine_sml1.
DR   Pfam; PF00048; IL8; 1.
DR   PRINTS; PR00437; SMALLCYTKCXC.
DR   SMART; SM00199; SCY; 1.
DR   PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
KW   Cytokine; Growth factor; Inflammatory response; Signal.
FT   SIGNAL       1     30        POTENTIAL.
FT   CHAIN        31    103       GROWTH REGULATED PROTEIN.
FT   DISULFID     39    65        BY SIMILARITY.
FT   DISULFID     41    81        BY SIMILARITY.
SQ   SEQUENCE   103 AA;  10820 MW;  C59857F346716695 CRC64;

  Query Match             21.7%;  Score 127.5;  DB 1;  Length 103;
  Best Local Similarity   34.4%;  Pred. No. 5.1e-07;
  Matches   33;  Conservative   16;  Mismatches   36;  Indels   11;  Gaps    2;

Qy          7 RAPPVSMRLLAAALLLLLLALYTARVDGS------KCKCSRKGPKIRYSDVKKLEMKPKY 60
              ||   : ||| ||:|||||     |  |:      :|:| :    |   ::: ::: |
Db          3 RAANPAPRLLGAAMLLLLLVAAGRRAAGAPVVNELRCQCLQTVQGIHLKNMQSVKVTPPG 62

Qy         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFI 96
              ||| :  || | |:     ||| ||:|     |: |
Db         63 PHCGQTEVIATLKT-----GQEVCLNPAAPMVKKII 93


RESULT 8
MIP2_RAT
ID   MIP2_RAT       STANDARD;      PRT;   100 AA.
AC   P30348;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Macrophage inflammatory protein 2 precursor (MIP2) (CINC-3).
GN   CXCL2 OR SCYB2 OR MIP2 OR MIP-2.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Fischer 344; TISSUE=Lung;
RA   Driscoll K.;
RL   Submitted (APR-1992) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Fischer;
RX   MEDLINE=95189993; PubMed=7883948;
RA   Feng L., Xia Y., Yoshimura T., Wilson C.B.;
RT   "Modulation of neutrophil influx in glomerulonephritis in the rat
RT   with anti-macrophage inflammatory protein-2 (MIP-2) antibody.";
RL   J. Clin. Invest. 95:1009-1017(1995).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CD Charles River; TISSUE=Lung;
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RA   Farone A., Farone M., Shi M.M., Kobzik L., Paulauskis J.D.;
RL   Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE OF 39-91 FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=93035653; PubMed=1415488;
RA   Huang S., Paulauskis J.D., Godleski J.J., Kobzik L.;
RT   "Expression of macrophage inflammatory protein-2 and KC mRNA in
RT   pulmonary inflammation.";
RL   Am. J. Pathol. 141:981-988(1992).
RN   [5]
RP   SEQUENCE OF 32-100.
RC   STRAIN=Wistar;
RX   MEDLINE=94318061; PubMed=8043001;
RA   Nakagawa H., Komorita N., Shibata F., Ikesue A., Konishi K.,
RA   Fujioka M., Kato H.;
RT   "Identification of cytokine-induced neutrophil chemoattractants
RT   (CINC), rat GRO/CINC-2 alpha and CINC-2 beta, produced by granulation
RT   tissue in culture: purification, complete amino acid sequences and
RT   characterization.";
RL   Biochem. J. 301:545-550(1994).
RN   [6]
RP   SEQUENCE OF 32-59.
RC   STRAIN=Wistar;
RX   MEDLINE=96183056; PubMed=8607872;
RA   Nakagawa H., Shiota S., Takano K., Shibata F., Kato H.;
RT   "Cytokine-induced neutrophil chemoattractant (CINC)-2 alpha, a novel
RT   member of rat GRO/CINCs, is a predominant chemokine produced by
RT   lipopolysaccharide-stimulated rat macrophages in culture.";
RL   Biochem. Biophys. Res. Commun. 220:945-948(1996).
CC   -!- FUNCTION: Chemotactic for human polymorphonuclear Leukocytes but
CC       does not induce chemokinesis or an oxidative burst. Contributes to
CC       neutrophil activation during inflammation.
CC   -!- SUBUNIT: Homotetramer.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: At least expressed in the lung and trachea.
CC   -!- INDUCTION: By lipopolysaccharide (LPS) and inflammation; in lung.
CC   -!- SIMILARITY: Belongs to the intercrine alpha (chemokine CxC)
CC       family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X65647; CAA46599.1; -.
DR   EMBL; S77604; AAB33749.1; -.
DR   EMBL; U45965; AAA92438.1; -.
DR   EMBL; S45855; -; NOT_ANNOTATED_CDS.
DR   PIR; S21467; S21467.
DR   HSSP; P10889; 1MI2.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   InterPro; IPR001089; CXC_chmkine_sml1.
DR   Pfam; PF00048; IL8; 1.
DR   PRINTS; PR00437; SMALLCYTKCXC.
DR   SMART; SM00199; SCY; 1.
DR   PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
KW   Cytokine; Chemotaxis; Inflammatory response; Signal.
FT   SIGNAL        1     31
FT   CHAIN        32    100       MACROPHAGE INFLAMMATORY PROTEIN 2.
FT   DISULFID     36     62       BY SIMILARITY.
FT   DISULFID     38     78       BY SIMILARITY.
SQ   SEQUENCE   100 AA;  10783 MW;  4299DFE68FF37A9B CRC64;

  Query Match             21.1%;  Score 124;  DB 1;  Length 100;
  Best Local Similarity   33.7%;  Pred. No. 1.2e-06;
  Matches   32;  Conservative   16;  Mismatches   37;  Indels   10;  Gaps    3;

Qy          8 APPVSMRLLAAALLLLLALY---TARVDGS--KCKCSRKGPKIRYSDVKKLEMKPKYPH 62
              |||     | |  :||||||     |  |  |  :|:|    |:: : ::: | : |  ||
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Db          2 APPTRQLLNAVLVLLLLLATNHQGTGVVVASELRCQCLTTLPRVDFKNIQSLTVTPPGPH 61

Qy         63 CEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIK 97
              | :  || | |      | | ||:|:    :| ::
Db         62 CAQTEVIATLKD-----GHEVCLNPEAPLVQRIVQ 91


RESULT 9
GROG_BOVIN
ID   GROG_BOVIN     STANDARD;      PRT;    98 AA.
AC   O46675;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Growth regulated protein homolog gamma precursor (GRO-gamma).
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99152612; PubMed=10028286;
RA   Modi W.S., Yoshimura T.;
RT   "Isolation of novel GRO genes and a phylogenetic analysis of the CXC
RT   chemokine subfamily in mammals.";
RL   Mol. Biol. Evol. 16:180-193(1999).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the intercrine alpha (chemokine CxC)
CC       family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U95811; AAB93927.1; -.
DR   HSSP; P19875; 1QNK.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   InterPro; IPR001089; CXC_chmkine_sml1.
DR   Pfam; PF00048; IL8; 1.
DR   PRINTS; PR00437; SMALLCYTKCXC.
DR   SMART; SM00199; SCY; 1.
DR   PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
KW   Cytokine; Growth factor; Inflammatory response; Signal.
FT   SIGNAL        1     29       POTENTIAL.
FT   CHAIN        30     98       GROWTH REGULATED PROTEIN HOMOLOG GAMMA.
FT   DISULFID     39     65       BY SIMILARITY.
FT   DISULFID     41     81       BY SIMILARITY.
SQ   SEQUENCE   98 AA;  10393 MW;  942CD6897C21EDE9 CRC64;

  Query Match             20.9%;  Score 122.5;  DB 1;  Length 98;
  Best Local Similarity   34.0%;  Pred. No. 1.7e-06;
  Matches   33;  Conservative   16;  Mismatches   35;  Indels   13;  Gaps    3;

Qy          8 APPVSM--RLLAAALLLLLLALYTARVDGS------KCKCSRKGPKIRYSDVKKLEMKPK 59
              ||  |   ||| ||:|||||      |  |:      :|:| :    |   ::: :::
Db          2 APAASSAPRLLRAAMLLLLLVAAGRRAAGAPVVNELRCQCLQTLQGIHLKNIQSVKVTTP 61

Qy         60 YPHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFI 96
                |||::  || | |:     ||| ||:|     |: |
Db         62 GPHCDQTEVIATLKT-----GQEVCLNPAAPMVKKII 93


RESULT 10
GRO2_RABIT
ID   GRO2_RABIT     STANDARD;      PRT;   104 AA.
AC   P47854;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
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DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Growth regulated protein homolog precursor (GRO homolog).
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Schwartz D., Chaverri-Alamada L., Berliner J., Kirchgessner T.,
RA   Quisomoro D., Fang J., Tekamp-Olson P., Lusis J., Fogelman A.,
RA   Territo M.;
RL   Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Plays a role in monocyte adhesion to the endothelium.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the intercrine alpha (chemokine CxC)
CC       family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U12310; AAA20487.1; -.
DR   HSSP; P19875; 1QNK.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   InterPro; IPR001089; CXC_chmkine_sml1.
DR   Pfam; PF00048; IL8; 1.
DR   PRINTS; PR00437; SMALLCYTKCXC.
DR   SMART; SM00199; SCY; 1.
DR   PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
KW   Cytokine; Growth factor; Inflammatory response; Signal.
FT   SIGNAL        1     31       PROBABLE.
FT   CHAIN        32    104       GROWTH REGULATED PROTEIN HOMOLOG.
FT   DISULFID     40     66       BY SIMILARITY.
FT   DISULFID     42     82       BY SIMILARITY.
SQ   SEQUENCE   104 AA;  10900 MW;  10B9D07B65C77F67 CRC64;

  Query Match             20.2%;  Score 118.5;  DB 1;  Length 104;
  Best Local Similarity   32.6%;  Pred. No. 5e-06;
  Matches   31;  Conservative   17;  Mismatches   36;  Indels   11;  Gaps    2;

Qy          8 APPVSMRLLAAALLLLLLALYTARVDGS------KCKCSRKGPKIRYSDVKKLEMKPKYP 61
              |   : |||  ||||||||      |  |:       :|:| :     |   ::: :::    |
Db          5 ATAAAPRLLRAALLLLLLVAAGRRAAGAPVVNELRCQCLQTLQGIHLKNIQSVKVTTPGP 64

Qy         62 HCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFI 96
              ||::  || : |:     ||| ||:|     |: |
Db         65 HCDQTEVIASLKT-----GQEVCLNPTAPVVKKII 94


RESULT 11
GROB_BOVIN
ID   GROB_BOVIN     STANDARD;      PRT;   104 AA.
AC   O46677;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Growth regulated protein homolog beta precursor (GRO-beta).
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99152612; PubMed=10028286;
RA   Modi W.S., Yoshimura T.;
RT   "Isolation of novel GRO genes and a phylogenetic analysis of the CXC
RT   chemokine subfamily in mammals.";
RL   Mol. Biol. Evol. 16:180-193(1999).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the intercrine alpha (chemokine CxC)
CC       family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U95813; AAB93929.1; -.
DR   HSSP; P19875; 1QNK.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   InterPro; IPR001089; CXC_chmkine_sml1.
DR   Pfam; PF00048; IL8; 1.
DR   PRINTS; PR00437; SMALLCYTKCXC.
DR   SMART; SM00199; SCY; 1.
DR   PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
KW   Cytokine; Growth factor; Inflammatory response; Signal.
FT   SIGNAL        1     30       POTENTIAL.
FT   CHAIN        31    104       GROWTH REGULATED PROTEIN HOMOLOG BETA.
FT   DISULFID     40     66       BY SIMILARITY.
FT   DISULFID     42     82       BY SIMILARITY.
SQ   SEQUENCE   104 AA;  10950 MW;  40A8C06A64D67F7B CRC64;

  Query Match             20.0%;  Score 117.5;  DB 1;  Length 104;
  Best Local Similarity   31.6%;  Pred. No. 6.4e-06;
  Matches   30;  Conservative   18;  Mismatches   36;  Indels   11;  Gaps    2;

Qy          8 APPVSMRLLAAALLLLLLALYTARVDGS------KCKCSRKGPKIRYSDVKKLEMKPKYP 61
              |   : |||  ||:|||||      |  |:       :|:| :     |   ::: :::    |
Db          5 ATAAAPRLLRAAMLLLLLVAAGRRAAGAPVVNELRCQCLQTLQGIHLKNIQSVKVTTPGP 64

Qy         62 HCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFI 96
              ||::  || : |:     ||| ||:|     |: |
Db         65 HCDQTEVIASLKT-----GQEVCLNPTAPMVKKII 94


RESULT 12
GRO_HUMAN
ID   GRO_HUMAN      STANDARD;      PRT;   107 AA.
AC   P09341;
DT   01-MAR-1989 (Rel. 10, Created)
DT   01-MAR-1989 (Rel. 10, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Growth regulated protein precursor (CXCL1) (Melanoma growth
DE   stimulatory activity) (MGSA) (Neutrophil-activating protein 3) (NAP-
DE   3).
GN   CXCL1 OR SCYB1 OR GRO1 OR GROA OR GRO OR MGSA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88041072; PubMed=2890161;
RA   Anisowicz A., Bardwell L., Sager R.;
RT   "Constitutive overexpression of a growth-regulated gene in
RT   transformed Chinese hamster and human cells.";
RL   Proc. Natl. Acad. Sci. U.S.A. 84:7188-7192(1987).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88328991; PubMed=2970963;
RA   Richmond A., Balentien E., Thomas H.G., Flaggs G., Barton D.E.,
RA   Spiess J., Bordoni R., Francke U., Derynck R.;
RT   "Molecular characterization and chromosomal mapping of melanoma
RT   growth stimulatory activity, a growth factor structurally related to
RT   beta-thromboglobulin.";
RL   EMBO J. 7:2025-2033(1988).
RN   [3]
RP   SEQUENCE FROM N.A.
```

```
RC   TISSUE=Blood;
RX   MEDLINE=91057157; PubMed=2129556;
RA   Baker N.E., Kucera G., Richmond A.;
RT   "Nucleotide sequence of the human melanoma growth stimulatory
RT   activity (MGSA) gene.";
RL   Nucleic Acids Res. 18:6453-6453(1990).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Ovary;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [5]
RP   SEQUENCE OF 35-65.
RX   MEDLINE=90217938; PubMed=2182761;
RA   Schroeder J.-M., Persoon N.L.M., Christophers E.;
RT   "Lipopolysaccharide-stimulated human monocytes secrete, apart from
RT   neutrophil-activating peptide 1/interleukin 8, a second neutrophil-
RT   activating protein. NH2-terminal amino acid sequence identity with
RT   melanoma growth stimulatory activity.";
RL   J. Exp. Med. 171:1091-1100(1990).
RN   [6]
RP   SEQUENCE OF 35-57.
RX   MEDLINE=89246368; PubMed=2655583;
RA   Golds E.E., Mason P., Nyirkos P.;
RT   "Inflammatory cytokines induce synthesis and secretion of gro protein
RT   and a neutrophil chemotactic factor but not beta 2-microglobulin in
RT   human synovial cells and fibroblasts.";
RL   Biochem. J. 259:585-588(1989).
RN   [7]
RP   POSSIBLE FUNCTION.
RX   MEDLINE=89356650; PubMed=2670560;
RA   Wen D., Rowland A., Derynck R.;
RT   "Expression and secretion of gro/MGSA by stimulated human endothelial
RT   cells.";
RL   EMBO J. 8:1761-1766(1989).
RN   [8]
RP   STRUCTURE BY NMR.
RX   MEDLINE=93387459; PubMed=8397104;
RA   Fairbrother W.J., Reilly D., Colby T., Horuk R.;
RT   "1H assignment and secondary structure determination of human
RT   melanoma growth stimulating activity (MGSA) by NMR spectroscopy.";
RL   FEBS Lett. 330:302-306(1993).
RN   [9]
RP   STRUCTURE BY NMR.
RX   MEDLINE=94376296; PubMed=8089846;
RA   Fairbrother W.J., Reilly D., Colby T., Hesselgesser J., Horuk R.;
RT   "The solution structure of melanoma growth stimulating activity.";
RL   J. Mol. Biol. 242:252-270(1994).
RN   [10]
RP   STRUCTURE BY NMR.
RX   MEDLINE=95105175; PubMed=7806518;
RA   Kim K.S., Clark-Lewis I., Sykes B.D.;
RT   "Solution structure of GRO/melanoma growth stimulatory activity
RT   determined by 1H NMR spectroscopy.";
RL   J. Biol. Chem. 269:32909-32915(1994).
CC   -!- FUNCTION: Has chemotactic activity for neutrophils. May play a
CC       role in inflammation and exerts its effects on endothelial cells
CC       in an autocrine fashion.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the intercrine alpha (chemokine CxC)
CC       family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; J03561; AAA35933.1; -.
DR   EMBL; X12510; CAA31027.1; -.
DR   EMBL; X54489; CAA38361.1; -.
DR   EMBL; BC011976; AAH11976.1; -.
DR   PIR; S13669; A28414.
DR   PDB; 1MGS; 30-SEP-94.
DR   PDB; 1MSG; 31-MAR-95.
DR   PDB; 1MSH; 31-MAR-95.
DR   PDB; 1ROD; 10-JUN-96.
DR   Genew; HGNC:4602; CXCL1.
DR   MIM; 155730; -.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0008009; F:chemokine activity; TAS.
DR   GO; GO:0008047; F:enzyme activator activity; TAS.
DR   GO; GO:0005102; F:receptor binding; TAS.
DR   GO; GO:0030036; P:actin cytoskeleton organization and biogenesis; TAS.
DR   GO; GO:0008283; P:cell proliferation; TAS.
DR   GO; GO:0006935; P:chemotaxis; TAS.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
DR   GO; GO:0006954; P:inflammatory response; TAS.
DR   GO; GO:0007242; P:intracellular signaling cascade; TAS.
DR   GO; GO:0008285; P:negative regulation of cell proliferation; TAS.
DR   GO; GO:0007401; P:pan-neural process; TAS.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   InterPro; IPR001089; CXC_chmkine_sm11.
DR   Pfam; PF00048; IL8; 1.
DR   PRINTS; PR00437; SMALLCYTKCXC.
DR   SMART; SM00199; SCY; 1.
DR   PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
KW   Cytokine; Growth factor; Inflammatory response; Signal; 3D-structure.
FT   SIGNAL       1     34
FT   CHAIN       35    107       GROWTH REGULATED PROTEIN.
FT   DISULFID     43     69
FT   DISULFID     45     85
FT   TURN         44     45
FT   STRAND       49     49
FT   TURN         54     56
FT   STRAND       57     63
FT   STRAND       73     78
FT   TURN         79     80
FT   STRAND       83     86
FT   TURN         88     89
FT   HELIX        91    103
FT   TURN        104    104
SQ   SEQUENCE   107 AA;  11301 MW;  17048A6B4D765CA2 CRC64;

  Query Match            20.0%;  Score 117.5;  DB 1;  Length 107;
  Best Local Similarity  32.3%;  Pred. No. 6.6e-06;
  Matches   31;  Conservative   17;  Mismatches   37;  Indels   11;  Gaps    2;

Qy          8 APPVSMRLLAAALLLLLLALYTARVDGS------KCKCSRKGPKIRYSDVKKLEMKPKYP 61
              | | : |||  |||||||      |  |:      :|:| :    |   ::: : :|  |
Db          8 AAPSNPRLLRVALLLLLLVAAGRRAAGASVATELRCQCLQTLQGIHPKNIQSVNVKSPGP 67

Qy         62 HCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIK 97
              || : || | |:     |:: ||:|     |: |:
Db         68 HCAQTEVIATLKN-----GRKACLNPASPIVKKIIE 98
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RESULT 13
MI2B_HUMAN
ID   MI2B_HUMAN      STANDARD;      PRT;   107 AA.
AC   P19876;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Macrophage inflammatory protein-2-beta precursor (MIP2-beta) (CXCL3)
DE   (Growth regulated protein gamma) (GRO-gamma).
GN   CXCL3 OR GRO3 OR SCYB3 OR GROG.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Histiocytic lymphoma;
RX   MEDLINE=90354792; PubMed=2201751;
RA   Tekamp-Olson P., Gallegos C., Bauer D., McClain J., Sherry B.,
RA   Fabre M., van Deventer S., Cerami A.;
RT   "Cloning and characterization of cDNAs for murine macrophage
RT   inflammatory protein 2 and its human homologues.";
RL   J. Exp. Med. 172:911-919(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91017578; PubMed=2217207;
RA   Haskill S., Peace A., Morris J., Sporn S.A., Anisowicz A., Lee S.W.,
RA   Smith T., Martin G., Ralph P., Sager R.;
RT   "Identification of three related human GRO genes encoding cytokine
RT   functions.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:7732-7736(1990).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: May play a role in inflammation and exert its effects on
CC       endothelial cells in an autocrine fashion.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the intercrine alpha (chemokine CxC)
CC       family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X53800; CAA37809.1; -.
DR   EMBL; M36821; AAA63184.1; -.
DR   EMBL; BC016308; AAH16308.1; -.
DR   PIR; JH0282; B38290.
DR   HSSP; P19875; 1QNK.
DR   Genew; HGNC:4604; CXCL3.
DR   MIM; 139111; -.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0008009; F:chemokine activity; TAS.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   InterPro; IPR001089; CXC_chmkine_sml1.
DR   Pfam; PF00048; IL8; 1.
DR   SMART; SM00199; SCY; 1.
DR   PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
KW   Cytokine; Chemotaxis; Inflammatory response; Signal.
FT   SIGNAL        1     34
FT   CHAIN        35    107       MACROPHAGE INFLAMMATORY PROTEIN-
FT                                 2-BETA.
FT   DISULFID     43     69       BY SIMILARITY.
FT   DISULFID     45     85       BY SIMILARITY.
FT   CONFLICT     27     28       AA -> G (IN REF. 2).
SQ   SEQUENCE   107 AA;  11342 MW;  97A69946B7F1F070 CRC64;

  Query Match             19.8%;  Score 116.5;  DB 1;  Length 107;
  Best Local Similarity   30.2%;  Pred. No. 8.4e-06;
  Matches   29;  Conservative   20;  Mismatches   36;  Indels   11;  Gaps    2;

Qy          8 APPVSMRLLAAALLLLLLALYTARVDGS------KCKCSRKGPKIRYSDVKKLEMKPKYP 61
              | | : |||  |||||||   : |  |:      :|:| :   |  ::: : ::  |
Db          8 AAPSNPRLLRVALLLLLLVAASRRAAGASVVTELRCQCLQTLQGIHLKNIQSVNVRSPGP 67

Qy         62 HCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIK 97
              || :  || | |:     |:: ||:|     :: |:
Db         68 HCAQTEVIATLKN-----GKKACLNPASPMVQKIIE 98


RESULT 14
GROA_BOVIN
ID   GROA_BOVIN      STANDARD;      PRT;   104 AA.
AC   O46676;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Growth regulated protein homolog alpha precursor (GRO-alpha).
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99152612; PubMed=10028286;
RA   Modi W.S., Yoshimura T.;
RT   "Isolation of novel GRO genes and a phylogenetic analysis of the CXC
RT   chemokine subfamily in mammals.";
RL   Mol. Biol. Evol. 16:180-193(1999).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the intercrine alpha (chemokine CxC)
CC       family.
CC   ---------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U95812; AAB93928.1; -.
DR   HSSP; P19875; 1QNK.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   InterPro; IPR001089; CXC_chmkine_sml1.
DR   Pfam; PF00048; IL8; 1.
DR   PRINTS; PR00437; SMALLCYTKCXC.
DR   SMART; SM00199; SCY; 1.
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DR   PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
KW   Cytokine; Growth factor; Inflammatory response; Signal.
FT   SIGNAL       1     30       POTENTIAL.
FT   CHAIN       31    104       GROWTH REGULATED PROTEIN HOMOLOG ALPHA.
FT   DISULFID    40     66       BY SIMILARITY.
FT   DISULFID    42     82       BY SIMILARITY.
SQ   SEQUENCE   104 AA;  10984 MW;  1002CAC064DB1F76 CRC64;

  Query Match             19.3%;  Score 113.5;  DB 1;  Length 104;
  Best Local Similarity   30.5%;  Pred. No. 1.7e-05;
  Matches   29;  Conservative   18;  Mismatches   37;  Indels   11;  Gaps    2;

Qy          8 APPVSMRLLAAALLLLLALYTARVDGS------KCKCSRKGPKIRYSDVKKLEMKPKYP 61
              |   : ||| ||:| |||      |  |:      :|:| :    |   ::: :::    |
Db          5 ATAAAPRLLRAAMLFLLLVAAGRRAAGAPVVNELRCQCLQTLQGIHLKNIQSVKVTTPGP 64

Qy         62 HCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFI 96
              ||::  || : |:     ||| ||:|     |: |
Db         65 HCDQTEVIASLKT-----GQEVCLNPTAPMVKKII 94


RESULT 15
GRO_MOUSE
ID   GRO_MOUSE      STANDARD;      PRT;    96 AA.
AC   P12850;
DT   01-OCT-1989 (Rel. 12, Created)
DT   01-OCT-1989 (Rel. 12, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Growth regulated protein precursor (CXCL1) (Platelet-derived growth
DE   factor-inducible protein KC) (Secretory protein N51).
GN   CXCL1 OR SCYB1 OR GRO1 OR GRO OR MGSA.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89139485; PubMed=2917992;
RA   Oquendo P., Alberta J., Wen D., Graycar J.L., Derynck R., Stiles C.D.;
RT   "The platelet-derived growth factor-inducible KC gene encodes a
RT   secretory protein related to platelet alpha-granule proteins.";
RL   J. Biol. Chem. 264:4133-4137(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89078502; PubMed=2909392;
RA   Ryseck R.P., Macdonald-Bravo H., Mattei M.-G., Bravo R.;
RT   "Cloning and sequence of a secretory protein induced by growth
RT   factors in mouse fibroblasts.";
RL   Exp. Cell Res. 180:266-275(1989).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/Sv;
RA   Bozic C.R., Kolakowski L.F. Jr., von Uexkull C., Garcia-Rodriguez M.,
RA   Conklyn M.J., Breslow R., Showell H.J., Gerard N.P., Gerard C.;
RL   Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE OF 1-10 FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=96016008; PubMed=7561058;
RA   Ohmori Y., Fukumoto S., Hamilton T.A.;
RT   "Two structurally distinct kappa B sequence motifs cooperatively
RT   control LPS-induced KC gene transcription in mouse macrophages.";
RL   J. Immunol. 155:3593-3600(1995).
CC   -!- FUNCTION: Has chemotactic activity for neutrophils. Contributes to
CC       neutrophil activation during inflammation (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- INDUCTION: By platelet-derived growth factor. In lung, by
CC       lipopolysaccharide or inflammation (By similarity).
CC   -!- SIMILARITY: Belongs to the intercrine alpha (chemokine CxC)
CC       family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J04596; AAA40131.1; -.
DR   EMBL; U20634; AAB03376.1; -.
DR   EMBL; U20527; AAB03376.1; JOINED.
DR   EMBL; S79767; -; NOT_ANNOTATED_CDS.
DR   PIR; A32954; A32954.
DR   HSSP; P19875; 1QNK.
DR   MGD; MGI:108068; Cxcl1.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   InterPro; IPR001089; CXC_chmkine_sml1.
DR   Pfam; PF00048; IL8; 1.
DR   PRINTS; PR00437; SMALLCYTKCXC.
DR   SMART; SM00199; SCY; 1.
DR   PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
KW   Cytokine; Growth factor; Inflammatory response; Signal.
FT   SIGNAL       1     24       PROBABLE.
FT   CHAIN       25     96       GROWTH REGULATED PROTEIN.
FT   DISULFID    33     59       BY SIMILARITY.
FT   DISULFID    35     75       BY SIMILARITY.
SQ   SEQUENCE   96 AA;  10254 MW;  4A52B5E5C38B45C2 CRC64;

  Query Match             18.9%;  Score 111;  DB 1;  Length 96;
  Best Local Similarity   30.8%;  Pred. No. 3e-05;
  Matches   28;  Conservative   18;  Mismatches   37;  Indels    8;  Gaps    2;

Qy         10 PVSMRLLAAALLLLL---LALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEK 66
              | :  || ||||||    ||       :  :|:| :    |   ::: |:: |  ||| :
Db          3 PATRSLLCAALLLLATSRLATGAPIANELRCQCLQTMAGIHLKNIQSLKVLPSGPHCTQT 62

Qy         67 MVIITTKSVSRYRGQEHCLHPKLQSTKRFIK 97
              || | |:     |:| || |:    :: ::
Db         63 EVIATLKN-----GREACLDPEAPLVQKIVQ 88


Search completed: April 22, 2004, 12:32:53
Job time : 18 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 22, 2004, 12:30:18 ; Search time 21 Seconds
(without alignments)
508.441 Million cell updates/sec

Title: US-09-978-189-370
Perfect score: 587
Sequence: 1 MSLLPRRAPPVSMRLLAAAL.....TKRFIKWYNAWNEKRRVYEE 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	520	88.6	99	2	JG0182	chemokine BRAK - h
2	143.5	24.4	100	2	S46198	cytokine-induced n
3	138	23.5	100	2	JH0200	macrophage inflamm
4	131	22.3	101	2	B28414	growth-regulated p
5	128.5	21.9	107	2	JH0281	macrophage inflamm
6	124	21.1	100	2	S21467	macrophage inflamm
7	124	21.1	100	2	I55614	macrophage inflamm
8	117.5	20.0	107	2	A28414	melanoma growth-st
9	116.5	19.8	107	2	B38290	GRO-gamma precurso
10	111	18.9	96	2	A32954	gro-alpha precurso
11	103	17.5	117	2	B44253	alveolar macrophag
12	97	16.5	96	2	JN0572	neutrophil chemo-a
13	94.5	16.1	126	2	A35766	platelet factor 4,
14	89	15.2	113	2	JC7800	neutrophil activat
15	87.5	14.9	125	2	JN0470	interferon gamma-i
16	85.5	14.6	53	2	I51886	macrophage inflamm
17	84	14.3	104	1	PFHU4A	platelet factor 4
18	82.5	14.1	103	2	A53096	interleukin-8 prec
19	82.5	14.1	128	1	TGHU	beta-thromboglobul
20	81.5	13.9	95	2	JN0841	interleukin-8 - do
21	81	13.8	101	1	PFHU4	platelet factor 4
22	80.5	13.7	53	2	I64831	gene KC protein -
23	80.5	13.7	98	2	A45492	IP-10 precursor -
24	80.5	13.7	103	2	A26736	transformation-ind
25	80.5	13.7	103	2	I50417	RSV-induced protei
26	80	13.6	119	2	S42881	platelet basic pro
27	79.5	13.5	98	1	TGHUGI	interferon gamma-i
28	79.5	13.5	101	2	S42496	interleukin-8 prec
29	76.5	13.0	114	2	A55010	neutrophil-activat
30	76	12.9	132	2	A57325	C-X-C chemokine LI
31	76	12.9	677	2	T27127	hypothetical prote
32	74	12.6	394	2	T32670	hypothetical prote
33	73.5	12.5	75	2	A54188	granulocyte chemot
34	73	12.4	105	2	A26774	platelet factor 4
35	72.5	12.4	101	2	I46871	interleukin-8 - ra
36	71.5	12.2	75	2	B54188	granulocyte chemot
37	71	12.1	99	2	A37034	interleukin-8 prec
38	71	12.1	1186	2	H88869	protein unc-31 [im
39	71	12.1	1270	2	T28087	hypothetical prote
40	70	11.9	308	1	S76941	carbamate kinase (
41	69.5	11.8	98	2	I59277	Mob-1 - rat
42	69.5	11.8	807	1	I51685	replication licens
43	68	11.6	149	2	T25246	hypothetical prote
44	68	11.6	309	2	S76393	hypothetical prote
45	68	11.6	581	2	C84251	flagella accessory

ALIGNMENTS

RESULT 1
JG0182
chemokine BRAK - human
C;Species: Homo sapiens (man)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 11-May-2000
C;Accession: JG0182
R;Hromas, R.; Broxmeyer, H.E.; Kim, C.; Nakshatri, H.; Christopherson II, K.; Hou, Y.
Biochem. Biophys. Res. Commun. 255, 703-706, 1999
A;Title: Cloning of BRAK, a novel divergent CXC chemokine preferentially expressed in no
A;Reference number: JG0182; MUID:99160416; PMID:10049774
A;Accession: JG0182
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-99 <HRO>
A;Cross-references: GB:AF073957
C;Superfamily: beta-thromboglobulin

Query Match 88.6%; Score 520; DB 2; Length 99;
Best Local Similarity 99.0%; Pred. No. 4.3e-47;
Matches 98; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy         13 MRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIITT 72
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRLPAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIITT 60

Qy         73 KSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
              ||||||||||||||||||||||||||||||||||||||||
Db         61 KSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 99
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RESULT 2
S46198
cytokine-induced neutrophil chemoattractant 2 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
C;Accession: S46198; C48988
R;Nakagawa, H.; Komorita, N.; Shibata, F.; Ikesue, A.; Konishi, K.; Fujioka, M.; Kato, H.
Biochem. J. 301, 545-550, 1994
A;Title: Identification of cytokine-induced neutrophil chemoattractants (CINC), rat GRO/C
ences and characterization.
A;Reference number: S46198; MUID:94318061; PMID:8043001
A;Accession: S46198
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-100 <NAK>
A;Cross-references: EMBL:D21095; NID:g517143; PIDN:BAA04657.1; PID:g517144
R;Nakagawa, H.; Ikesue, A.; Hatakeyama, S.; Kato, H.; Gotoda, T.; Komorita, N.; Watanabe,
Biochem. Pharmacol. 45, 1425-1430, 1993
A;Title: Production of an interleukin-8-like chemokine by cytokine-stimulated rat NRK-49
A;Reference number: A48988; MUID:93228656; PMID:8471066
A;Accession: C48988
A;Status: preliminary

A;Molecule type: protein
A;Residues: 33-56 <NA2>
A;Experimental source: kidney, NRK-49F fibroblasts
A;Note: sequence extracted from NCBI backbone (NCBIP:129130)
C;Superfamily: beta-thromboglobulin

Query Match 24.4%; Score 143.5; DB 2; Length 100;
Best Local Similarity 35.1%; Pred. No. 7.6e-08;
Matches 34; Conservative 19; Mismatches 31; Indels 13; Gaps 3;

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Qy          8 APPVSMRLLAAALLLLLLALYTARVDGS-------KCKCSRKGPKIRYSDVKKLEMKPKY 60
              ||| : ||| |||||||| : |:           :|:| :  |:: : ::: | : |
Db          2 APP-TRRLLNAALLLLLLLMATSHQPSGTVVARELRCQCLKTLPRVDFENIQSLTVTPPG 60

Qy         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIK 97
              ||| :  || | |      ||| ||:|:    :: |:
Db         61 PHCTQTEVIATLKD-----GQEVCLNPQAPRLQKIIQ 92
```

RESULT 3
JH0200
macrophage inflammatory protein 2 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 20-Aug-1999
C;Accession: JH0200; A32190
R;Tekamp-Olson, P.; Gallegos, C.; Bauer, D.; McClain, J.; Sherry, B.; Fabre, M.; van Dev
J. Exp. Med. 172, 911-919, 1990
A;Title: Cloning and characterization of cDNAs for murine macrophage inflammatory protei
A;Reference number: JH0200; MUID:90354792; PMID:2201751
A;Accession: JH0200
A;Molecule type: mRNA
A;Residues: 1-100 <TEK>
A;Cross-references: GB:X53798; NID:g53128; PIDN:CAA37807.1; PID:g53129
R;Wolpe, S.D.; Sherry, B.; Juers, D.; Davatelis, G.; Yurt, R.W.; Cerami, A.
Proc. Natl. Acad. Sci. U.S.A. 86, 612-616, 1989
A;Title: Identification and characterization of macrophage inflammatory protein 2.
A;Reference number: A32190; MUID:89098980; PMID:2643119
A;Accession: A32190
A;Molecule type: protein
A;Residues: 28-59 <WOL>
C;Superfamily: beta-thromboglobulin
C;Keywords: heparin binding
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-100/Product: macrophage inflammatory protein 2 #status experimental <MAT>

Query Match 23.5%; Score 138; DB 2; Length 100;
Best Local Similarity 33.3%; Pred. No. 2.9e-07;
Matches 32; Conservative 21; Mismatches 31; Indels 12; Gaps 3;

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Qy          8 APPVSMRLLAAALLLLLLALYTARVDGS------KCKCSRKGPKIRYSDVKKLEMKPKYP 61
              ||| : |||:|||:|||     :  |:      :|:| :  |:: : ::: | : |  |
Db          2 APP-TCRLLSAALVLLLLLATNHQATGAVVASELRCQCLKTLPRVDFKNIQSLSVTPPGP 60

Qy         62 HCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIK 97
              || :  || | |      ||: || |:    :: |:
Db         61 HCAQTEVIATLKG-----GQKVCLDPEAPLVQKIIQ 91
```

RESULT 4
B28414
growth-regulated protein precursor - Chinese hamster
C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 20-Aug-1999
C;Accession: B28414
R;Anisowicz, A.; Bardwell, L.; Sager, R.
Proc. Natl. Acad. Sci. U.S.A. 84, 7188-7192, 1987
A;Title: Constitutive overexpression of a growth-regulated gene in transformed Chinese h
A;Reference number: A94184; MUID:88041072; PMID:2890161
A;Accession: B28414
A;Molecule type: mRNA
A;Residues: 1-101 <ANI>
A;Cross-references: GB:J03560; NID:g191088; PIDN:AAA36985.1; PID:g304509
A;Note: the authors translated the codon CAG for residue 52 as Glu

C;Superfamily: beta-thromboglobulin
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-101/Product: growth-regulated protein #status predicted <MAT>

Query Match 22.3%; Score 131; DB 2; Length 101;
Best Local Similarity 31.6%; Pred. No. 1.5e-06;
Matches 30; Conservative 21; Mismatches 32; Indels 12; Gaps 2;

```
Qy         10 PVSMRLLAAALLLLLLALYTARV-------DGSKCKCSRKGPKIRYSDVKKLEMKPKYPH 62
              | :  || | |||||| | |:|:       :  :|:| :    :   ::: |:: |  ||
Db          3 PATRSLLRAPLLLLLLLATSRLATGAPVANELRCQCLQTMTGVHLKNIQSLKVTPPGPH 62

Qy         63 CEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIK 97
              | :  || | |:      ||| ||:|:    :: ::
Db         63 CTQTEVIATLKN-----GQEACLNPEAPMVQKIVQ 92
```

RESULT 5
JH0281
macrophage inflammatory protein 2 alpha precursor - human
N;Alternate names: gro-beta; growth regulated protein beta; melanoma growth-stimulatory a
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 20-Aug-1999
C;Accession: JH0281; A35931; A38290; A60407
R;Tekamp-Olson, P.; Gallegos, C.; Bauer, D.; McClain, J.; Sherry, B.; Fabre, M.; van Deve
J. Exp. Med. 172, 911-919, 1990
A;Title: Cloning and characterization of cDNAs for murine macrophage inflammatory protein
A;Reference number: JH0200; MUID:90354792; PMID:2201751
A;Accession: JH0281
A;Molecule type: mRNA
A;Residues: 1-107 <TEK>
A;Cross-references: GB:X53799; NID:g34658; PIDN:CAA37808.1; PID:g34659
R;Iida, N.; Grotendorst, G.R.
Mol. Cell. Biol. 10, 5596-5599, 1990
A;Title: Cloning and sequencing of a new gro transcript from activated human monocytes: e
A;Reference number: A35931; MUID:90377259; PMID:2078213
A;Accession: A35931
A;Molecule type: mRNA
A;Residues: 1-107 <IID>
A;Cross-references: GB:M57731; GB:M36964; NID:g183626; PIDN:AAA63182.1; PID:g183627
R;Haskill, S.; Peace, A.; Morris, J.; Sporn, S.A.; Anisowicz, A.; Lee, S.W.; Smith, T.; M
Proc. Natl. Acad. Sci. U.S.A. 87, 7732-7736, 1990
A;Title: Identification of three related human GRO genes encoding cytokine functions.
A;Reference number: A38290; MUID:91017578; PMID:2217207
A;Accession: A38290
A;Molecule type: mRNA
A;Residues: 1-107 <HAS>
A;Cross-references: GB:M36820; NID:g183628; PIDN:AAA63183.1; PID:g183629
R;Sporn, S.A.; Eierman, D.F.; Johnson, C.E.; Morris, J.; Martin, G.; Ladner, M.; Haskill,
J. Immunol. 144, 4434-4441, 1990
A;Title: Monocyte adherence results in selective induction of novel genes sharing homolog
A;Reference number: A60407; MUID:90257367; PMID:2341726
A;Accession: A60407
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 56-107 <SPO>
C;Superfamily: beta-thromboglobulin
C;Keywords: inflammation
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-107/Product: macrophage inflammatory protein 2 alpha #status predicted <MAT>

Query Match 21.9%; Score 128.5; DB 2; Length 107;
Best Local Similarity 33.3%; Pred. No. 3e-06;
Matches 32; Conservative 18; Mismatches 35; Indels 11; Gaps 2;

```
Qy          8 APPVSMRLLAAALLLLLLALYTARVDGS------KCKCSRKGPKIRYSDVKKLEMKPKYP 61
              | | : |||  |||||||   :  |  |:      :|:| :    |   ::: :::|   |
Db          8 AAPSNPRLLRVALLLLLLVAASRRAAGAPLATELRCQCLQTLQGIHLKNIQSVKVKSPGP 67

Qy         62 HCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIK 97
              || :  || | |:      ||: ||:|      |: |:
Db         68 HCAQTEVIATLKN-----GQKACLNPASPMVKKIIE 98
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RESULT 6
S21467
macrophage inflammatory protein 2 - rat
N;Alternate names: chemoattractant P-1
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Aug-1999
C;Accession: S21467; D48988
R;Driscoll, K.
submitted to the EMBL Data Library, April 1992
A;Reference number: S21467
A;Accession: S21467
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-100 <DRI>
A;Cross-references: EMBL:X65647; NID:g56665; PIDN:CAA46599.1; PID:g56666
R;Nakagawa, H.; Ikesue, A.; Hatakeyama, S.; Kato, H.; Gotoda, T.; Komorita, N.; Watanabe
Biochem. Pharmacol. 45, 1425-1430, 1993
A;Title: Production of an interleukin-8-like chemokine by cytokine-stimulated rat NRK-49
A;Reference number: A48988; MUID:93228656; PMID:8471066
A;Accession: D48988
A;Status: preliminary
A;Molecule type: protein
A;Residues: 32-45 <NAK>
A;Experimental source: kidney, NRK-49F fibroblasts
A;Note: sequence extracted from NCBI backbone (NCBIP:129129)
C;Superfamily: beta-thromboglobulin

Query Match 21.1%; Score 124; DB 2; Length 100;
Best Local Similarity 33.7%; Pred. No. 8.2e-06;
Matches 32; Conservative 16; Mismatches 37; Indels 10; Gaps 3;

Qy 8 APPVSMRLLAAALLLLLALY---TARVDGS--KCKCSRKGPKIRYSDVKKLEMKPKYPH 62
Db 2 APPTRQLLNAVLVLLLLLATNHQGTGVVVASELRCQCLTTLPRVDFKNIQSLTVTPPGPH 61

Qy 63 CEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIK 97
Db 62 CAQTEVIATLKD-----GHEVCLNPEAPLVQRIVQ 91

RESULT 7
I55614
macrophage inflammatory protein-2 - rat
C;Species: Rattus sp. (rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 20-Aug-1999
C;Accession: I55614
R;Feng, L.; Xia, Y.; Yoshimura, T.; Wilson, C.B.
J. Clin. Invest. 95, 1009-1017, 1995
A;Title: Modulation of neutrophil influx in glomerulonephritis in the rat with anti-macr
A;Reference number: I55614; MUID:95189993; PMID:7883948
A;Accession: I55614
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-100 <RES>
A;Cross-references: GB:S77604; NID:g998406; PIDN:AAB33749.1; PID:g998407
C;Superfamily: beta-thromboglobulin

Query Match 21.1%; Score 124; DB 2; Length 100;
Best Local Similarity 33.7%; Pred. No. 8.2e-06;
Matches 32; Conservative 16; Mismatches 37; Indels 10; Gaps 3;

Qy 8 APPVSMRLLAAALLLLLALY---TARVDGS--KCKCSRKGPKIRYSDVKKLEMKPKYPH 62
Db 2 APPTRQLLNAVLVLLLLLATNHQGTGVVVASELRCQCLTTLPRVDFKNIQSLTVTPPGPH 61

Qy 63 CEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIK 97
Db 62 CAQTEVIATLKD-----GHEVCLNPEAPLVQRIVQ 91

RESULT 8
A28414
melanoma growth-stimulatory activity precursor - human
N;Alternate names: fibroblast-derived neutrophil-activating protein gamma; GRO-alpha; grc
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 20-Aug-1999
C;Accession: S13669; A28414; S00983; B60401; S03976; A47626; B46519
R;Baker, N.E.; Kucera, G.; Richmond, A.
Nucleic Acids Res. 18, 6453, 1990
A;Title: Nucleotide sequence of the human melanoma growth stimulatory activity (MGSA) ger
A;Reference number: S13669; MUID:91057157; PMID:2129556
A;Accession: S13669
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-107 <BAK>
A;Cross-references: EMBL:X54489; NID:g34625; PIDN:CAA38361.1; PID:g34626
R;Anisowicz, A.; Bardwell, L.; Sager, R.
Proc. Natl. Acad. Sci. U.S.A. 84, 7188-7192, 1987
A;Title: Constitutive overexpression of a growth-regulated gene in transformed Chinese ha
A;Reference number: A94184; MUID:88041072; PMID:2890161
A;Accession: A28414
A;Molecule type: mRNA
A;Residues: 1-107 <ANI>
A;Cross-references: GB:J03561; NID:g183622; PIDN:AAA35933.1; PID:g306806
R;Richmond, A.; Balentien, E.; Thomas, H.G.; Flaggs, G.; Barton, D.E.; Spiess, J.; Bordor
EMBO J. 7, 2025-2033, 1988
A;Title: Molecular characterization and chromosomal mapping of melanoma growth stimulator
A;Reference number: S00983; MUID:88328991; PMID:2970963
A;Accession: S00983
A;Molecule type: mRNA
A;Residues: 1-107 <RIC>
A;Cross-references: EMBL:X12510; NID:g34621; PIDN:CAA31027.1; PID:g34622
R;Schroeder, J.M.; Sticherling, M.; Henneicke, H.H.; Preissner, W.C.; Christophers, E.
J. Immunol. 144, 2223-2232, 1990
A;Title: IL-1alpha or tumor necrosis factor-alpha stimulate release of three NAP-1/IL-8-1
A;Reference number: A60401; MUID:90187866; PMID:2179408
A;Accession: B60401
A;Molecule type: protein
A;Residues: 35-42,'X',44,'X',46-48 <SCH>
A;Experimental source: dermal fibroblasts
R;Golds, E.E.; Mason, P.; Nyirkos, P.
Biochem. J. 259, 585-588, 1989
A;Title: Inflammatory cytokines induce synthesis and secretion of gro protein and a neut
A;Reference number: S03975; MUID:89246368; PMID:2655583
A;Accession: S03976
A;Molecule type: protein
A;Residues: 35-41,'X',43-49,'X',51-52,'XX',55-57 <GOL>
R;Schroeder, J.M.; Persoon, N.L.M.; Christophers, E.
J. Exp. Med. 171, 1091-1100, 1990
A;Title: Lipopolysaccharide-stimulated human monocytes secrete, apart from neutrophil-act
ntity with melanoma growth stimulatory activity.
A;Reference number: A47626; MUID:90217938; PMID:2182761
A;Accession: A47626
A;Molecule type: protein
A;Residues: 35-63,'X',65 <SC2>
A;Experimental source: LPS-stimulated monocytes
R;Proost, P.; De Wolf-Peeters, C.; Conings, R.; Opdenakker, G.; Billiau, A.; Van Damme,
J. Immunol. 150, 1000-1010, 1993
A;Title: Identification of a novel granulocyte chemotactic protein (GCP-2) from human tun
A;Reference number: A46519; MUID:93139489; PMID:8423327
A;Accession: B46519
A;Molecule type: protein
A;Residues: 35-62 <PRO>
A;Experimental source: MG-63 osteosarcoma cells
C;Genetics:
A;Gene: GDB:GRO1
A;Cross-references: GDB:120181; OMIM:155730
A;Map position: 4q21-4q21
C;Superfamily: beta-thromboglobulin
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-107/Product: melanoma growth-stimulatory activity #status experimental <MAT>

Query Match 20.0%; Score 117.5; DB 2; Length 107;
Best Local Similarity 32.3%; Pred. No. 4.2e-05;
Matches 31; Conservative 17; Mismatches 37; Indels 11; Gaps 2;

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Qy          8 APPVSMRLLAAALLLLLLALYTARVDGS------KCKCSRKGPKIRYSDVKKLEMKPKYP 61
              | | : |||  |||||||     |  |:      :|:| :     |  ::: : :|   |
Db          8 AAPSNPRLLRVALLLLLLVAAGRRAAGASVATELRCQCLQTLQGIHPKNIQSVNVKSPGP 67

Qy         62 HCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIK 97
              || :  || | |:     |:: ||:|     |: |:
Db         68 HCAQTEVIATLKN-----GRKACLNPASPIVKKIIE 98


RESULT 9
B38290
GRO-gamma precursor - human
N;Alternate names: growth-regulated protein gamma; macrophage inflammatory protein 2 bet
C;Species: Homo sapiens (man)
C;Date: 31-May-1991 #sequence_revision 27-Oct-1995 #text_change 20-Aug-1999
C;Accession: JH0282; B38290; C46519
R;Tekamp-Olson, P.; Gallegos, C.; Bauer, D.; McClain, J.; Sherry, B.; Fabre, M.; van Dev
J. Exp. Med. 172, 911-919, 1990
A;Title: Cloning and characterization of cDNAs for murine macrophage inflammatory protei
A;Reference number: JH0200; MUID:90354792; PMID:2201751
A;Accession: JH0282
A;Molecule type: mRNA
A;Residues: 1-107 <TEK>
A;Cross-references: GB:X53800; NID:g34662; PIDN:CAA37809.1; PID:g34663
R;Haskill, S.; Peace, A.; Morris, J.; Sporn, S.A.; Anisowicz, A.; Lee, S.W.; Smith, T.;
Proc. Natl. Acad. Sci. U.S.A. 87, 7732-7736, 1990
A;Title: Identification of three related human GRO genes encoding cytokine functions.
A;Reference number: A38290; MUID:91017578; PMID:2217207
A;Accession: B38290
A;Molecule type: mRNA
A;Residues: 1-26,'G',29-107 <HAS>
A;Cross-references: GB:M36821; NID:g183632; PIDN:AAA63184.1; PID:g183633
R;Proost, P.; De Wolf-Peeters, C.; Conings, R.; Opdenakker, G.; Billiau, A.; Van Damme,
J. Immunol. 150, 1000-1010, 1993
A;Title: Identification of a novel granulocyte chemotactic protein (GCP-2) from human tu
A;Reference number: A46519; MUID:93139489; PMID:8423327
A;Accession: C46519
A;Molecule type: protein
A;Residues: 35-52 <PRO>
A;Experimental source: MG-63 osteosarcoma cells
C;Genetics:
A;Map position: 4q21
C;Superfamily: beta-thromboglobulin
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-107/Product: GRO-gamma #status experimental <MAT>

  Query Match             19.8%;  Score 116.5;  DB 2;  Length 107;
  Best Local Similarity   30.2%;  Pred. No. 5.3e-05;
  Matches   29;  Conservative   20;  Mismatches   36;  Indels   11;  Gaps    2;

Qy          8 APPVSMRLLAAALLLLLLALYTARVDGS------KCKCSRKGPKIRYSDVKKLEMKPKYP 61
              | | : |||  |||||||     : |  |:      :|:| :     |  ::: : ::   |
Db          8 AAPSNPRLLRVALLLLLLVAASRRAAGASVVTELRCQCLQTLQGIHLKNIQSVNVRSPGP 67

Qy         62 HCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIK 97
              || :  || | |:     |:: ||:|     :: |:
Db         68 HCAQTEVIATLKN-----GKKACLNPASPMVQKIIE 98


RESULT 10
A32954
gro-alpha precursor - mouse
N;Alternate names: gro protein; growth regulated protein; melanoma growth-stimulating ac
C;Species: Mus musculus (house mouse)
C;Date: 20-Oct-1989 #sequence_revision 20-Oct-1989 #text_change 20-Aug-1999
C;Accession: A32954; JH0081
R;Oquendo, P.; Alberta, J.; Wen, D.; Graycar, J.L.; Derynck, R.; Stiles, C.D.
J. Biol. Chem. 264, 4133-4137, 1989
A;Title: The platelet-derived growth factor-inducible KC gene encodes a secretory protei
A;Reference number: A32954; MUID:89139485; PMID:2917992
A;Accession: A32954
A;Molecule type: mRNA
A;Residues: 1-96 <OQU>
A;Cross-references: GB:J04596; NID:g201042; PIDN:AAA40131.1; PID:g201043
R;Ryseck, R.P.; MacDonald-Bravo, H.; Mattei, M.G.; Bravo, R.
Exp. Cell Res. 180, 266-275, 1989
A;Title: Cloning and sequence of a secretory protein induced by growth factors in mouse f
A;Reference number: JH0081; MUID:89078502; PMID:2909392
A;Accession: JH0081
A;Molecule type: mRNA
A;Residues: 1-96 <RYS>
C;Comment: This protein is basic and lacks threonine, phenylalanine, and tyrosine.
C;Genetics:
A;Map position: 5
C;Superfamily: beta-thromboglobulin
C;Keywords: extracellular protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-96/Product: gro-alpha #status predicted <MAT>

  Query Match             18.9%;  Score 111;  DB 2;  Length 96;
  Best Local Similarity   30.8%;  Pred. No. 0.00018;
  Matches   28;  Conservative   18;  Mismatches   37;  Indels    8;  Gaps    2;

Qy         10 PVSMRLLAAALLLLL---LALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEK 66
              | :  || ||||||     ||       :  :|:| :     |    ::: |:: |  ||| :
Db          3 PATRSLLCAALLLLATSRLATGAPIANELRCQCLQTMAGIHLKNIQSLKVLPSGPHCTQT 62

Qy         67 MVIITTKSVSRYRGQEHCLHPKLQSTKRFIK 97
              || | |:     |:| || |:    :: ::
Db         63 EVIATLKN-----GREACLDPEAPLVQKIVQ 88


RESULT 11
B44253
alveolar macrophage chemotactic factor-II (AMCF-II) intercrine-alpha protein - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 20-Aug-1999
C;Accession: B44253
R;Goodman, R.B.; Foster, D.C.; Mathewes, S.L.; Osborn, S.G.; Kuijper, J.L.; Forstrom, J.W
Biochemistry 31, 10483-10490, 1992
A;Title: Molecular cloning of porcine alveolar macrophage-derived neutrophil chemotactic
A;Reference number: A44253; MUID:93041741; PMID:1420165
A;Accession: B44253
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 1-117 <GOO>
A;Cross-references: GB:M99368; NID:g164325; PIDN:AAA30991.1; PID:g164326
A;Experimental source: alveolar macrophage
A;Note: sequence extracted from NCBI backbone (NCBIN:117417, NCBIP:117418)
C;Superfamily: beta-thromboglobulin

  Query Match             17.5%;  Score 103;  DB 2;  Length 117;
  Best Local Similarity   31.2%;  Pred. No. 0.0015;
  Matches   35;  Conservative   11;  Mismatches   46;  Indels   20;  Gaps    3;

Qy          1 MSLLPRRAP--PVSMRLLAAALLLLL-------------ALYTARVDGSKCKCSRKGPK 45
              | ||  ||    |    ||  | | :|||             |   | |   :| |    |
Db          1 MRLLTSRATRVPSPSGLLCAVLAMLLLTPSGPLASASPIEAAEAAVVRELRCMCLTTTPG 60

Qy         46 IRYSDVKKLEMKPKYPHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIK 97
              |    :  |:: |  | | :  || | |:     |:| || ||    |: ::
Db         61 IHPKMISDLQVIPAGPQCSKAEVIATLKN-----GKEVCLDPKAPLIKKIVQ 107


RESULT 12
JN0572
neutrophil chemo-attractant Gro protein precursor - rat
N;Alternate names: CINC; cytokine-induced neutrophil chemoattractant; interleukin-8-like
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Jun-2000
C;Accession: JN0572; JQ1519; A34481; A48988; B48988; S51214
R;Konishi, K.; Takata, Y.; Yamamoto, M.; Yomogida, K.; Watanabe, K.; Tsurufuji, S.; Fujic
Gene 126, 285-286, 1993
A;Title: Structure of the gene encoding rat neutrophil chemo-attractant Gro.
A;Reference number: JN0572; MUID:93246259; PMID:8482545
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A;Accession: JN0572
A;Molecule type: DNA
A;Residues: 1-96 <KON>
A;Cross-references: DDBJ:D11445; NID:g391854; PIDN:BAA02009.1; PID:g220755
R;Huang, S.; Paulauskis, J.D.; Kobzik, L.
Biochem. Biophys. Res. Commun. 184, 922-929, 1992
A;Title: Rat KC cDNA cloning and mRNA expression in lung macrophages and fibroblasts.
A;Reference number: JQ1519; MUID:92246987; PMID:1374243
A;Accession: JQ1519
A;Molecule type: mRNA
A;Residues: 1-32,'S',34-96 <HUA>
A;Cross-references: GB:M86536
A;Experimental source: alveolar macrophage
A;Note: the authors translated the codon AGT for residue 33 as Cys, AAC for residue 46 a
R;Watanabe, K.; Konishi, K.; Fujioka, M.; Kinoshita, S.; Nakagawa, H.
J. Biol. Chem. 264, 19559-19563, 1989
A;Title: The neutrophil chemoattractant produced by the rat kidney epithelioid cell line
A;Reference number: A34481; MUID:90062049; PMID:2684956
A;Accession: A34481
A;Molecule type: protein
A;Residues: 25-96 <WAT>
R;Nakagawa, H.; Ikesue, A.; Hatakeyama, S.; Kato, H.; Gotoda, T.; Komorita, N.; Watanabe
Biochem. Pharmacol. 45, 1425-1430, 1993
A;Title: Production of an interleukin-8-like chemokine by cytokine-stimulated rat NRK-49
A;Reference number: A48988; MUID:93228656; PMID:8471066
A;Accession: A48988
A;Status: preliminary
A;Molecule type: protein
A;Residues: 25-57 <NAK>
A;Experimental source: kidney, NRK-49F fibroblasts
A;Note: sequence extracted from NCBI backbone (NCBIP:129132)
A;Accession: B48988
A;Status: preliminary
A;Molecule type: protein
A;Residues: 25-57 <NA2>
A;Experimental source: kidney, NRK-49F fibroblasts
A;Note: sequence extracted from NCBI backbone (NCBIP:129131)
R;Hanzawa, H.; Haruyama, H.; Watanabe, K.; Tsurufuji, S.
FEBS Lett. 354, 207-212, 1994
A;Title: The three dimensional structure of rat cytokine CINC/Gro in solution by homonuc
A;Reference number: S51214; MUID:95046335; PMID:7957925
A;Contents: annotation; conformation by (1)H-NMR, residues 25-96
A;Accession: S51214
A;Molecule type: protein
A;Residues: 25-96 <HAN>
C;Comment: This protein has chemotactic activity for neutrophils and has melanoma growth
C;Genetics:
A;Gene: gro; KC
A;Introns: 24/1; 65/2; 92/2
C;Superfamily: beta-thromboglobulin
C;Keywords: cytokine; disulfide bond
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-96/Product: neutrophil chemo-attractant Gro protein #status experimental <CYT>

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Matches 25; Conservative 20; Mismatches 29; Indels 16; Gaps 3;

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Db          8 LLCAALPVLA----TSRQATGAPVANELRCQCLQTVAGIHFKNIQSLKVMPPGPHCTQTE 63

Qy         68 VIITTKSVSRYRGQEHCLHPKLQSTKRFIK 97
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Db         64 VIATLKN-----GREACLDPEAPMVQKIVQ 88
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platelet factor 4, interferon gamma-induced, precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 05-Oct-1990 #sequence_revision 05-Oct-1990 #text_change 20-Aug-1999
C;Accession: A35766
R;Farber, J.M.
Proc. Natl. Acad. Sci. U.S.A. 87, 5238-5242, 1990
A;Title: A macrophage mRNA selectively induced by gamma-interferon encodes a member of th
A;Reference number: A35766; MUID:90319087; PMID:2115167
A;Accession: A35766
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-126 <FAR>
A;Cross-references: GB:M34815; NID:g199692; PIDN:AAA39706.1; PID:g199693
C;Superfamily: beta-thromboglobulin

Query Match 16.1%; Score 94.5; DB 2; Length 126;
Best Local Similarity 25.5%; Pred. No. 0.012;
Matches 26; Conservative 21; Mismatches 40; Indels 15; Gaps 4;

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Db          1 MKSAVLFLLGIIFLEQCGVRGTLVIRNARCSCISTSRGTIHYKSLKDLKQFAPSPNCNKT 60

Qy         67 MVIITTKSVSRYRGQEHCLHPKLQSTKRFIK-WYNAWNEKRR 107
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RESULT 14
JC7800
neutrophil activating peptide-2 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Apr-2002 #sequence_revision 02-Apr-2002 #text_change 02-Apr-2002
C;Accession: JC7800
R;Oda, M.; Haruta, H.; Nagao, M.; Nagata, Y.
Biochem. Biophys. Res. Commun. 290, 865-868, 2002
A;Title: Isolation and characterization of mouse homolog of the neutrophil activating pep
A;Reference number: JC7800
A;Contents: Megakaryocyte
A;Accession: JC7800
A;Molecule type: mRNA
A;Residues: 1-113 <ODA>
A;Cross-references: DDBJ:AB042817
C;Comment: This protein is highly basic, and is specifically induced by thrombopoietin st
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C;Genetics:
A;Gene: nap-2

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Db         23 LLLLGLILVALAPLTAGKSDGMDPYIELRCRCTNTISGIPFNSISLVNVYRPGVHCADVE 82

Qy         68 VIITTKSVSRYRGQEHCLHPKLQSTKRFI 96
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Db         83 VIATLKN-----GQKTCLDPNAPGVKRIV 106
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RESULT 15
JN0470
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C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 28-May-1999
C;Accession: JN0470
R;Farber, J.M.
Biochem. Biophys. Res. Commun. 192, 223-230, 1993
A;Title: HuMig: a new human member of the chemokine family of cytokines.
A;Reference number: JN0470; MUID:93236577; PMID:8476424
A;Accession: JN0470
A;Molecule type: mRNA
A;Residues: 1-125 <FAR>
A;Cross-references: GB:X72755; GB:S60728; NID:g311375; PIDN:CAA51284.1; PID:g311376
C;Superfamily: beta-thromboglobulin
C;Keywords: cytokine

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Db          9 LLGIILLVLIGVQGTPVVRKGRCSCISTNQGTIHLQSLKDLKQFAPSPSCEKIEIIATLK 68

Qy         74 SVSRYRGQEHCLHPKLQSTKRFI-KWYNAWNEKRR 107
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Db         69 N-----GVQTCLNPDSADVKELIKKWEKQVSQKK 98
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Job time : 22 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 22, 2004, 12:33:53 ; Search time 42 Seconds
(without alignments)
730.684 Million cell updates/sec

Title: US-09-978-189-370
Perfect score: 587
Sequence: 1 MSLLPRRAPPVSMRLLAAAL.....TKRFIKWYNAWNEKRRVYEE 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1133595 seqs, 276475211 residues

Total number of hits satisfying chosen parameters: 1133595

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	587	100.0	111	9	US-09-816-920-2	Sequence 2, Appli
2	587	100.0	111	9	US-09-978-295A-370	Sequence 370, App
3	587	100.0	111	9	US-09-978-697-370	Sequence 370, App
4	587	100.0	111	9	US-09-978-192A-370	Sequence 370, App
5	587	100.0	111	9	US-09-999-832A-370	Sequence 370, App
6	587	100.0	111	10	US-09-978-189-370	Sequence 370, App
7	587	100.0	111	10	US-09-978-608A-370	Sequence 370, App
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ALIGNMENTS

RESULT 1
US-09-816-920-2
; Sequence 2, Application US/09816920
; Patent No. US20020119118A1
; GENERAL INFORMATION:
; APPLICANT: Fong,Sherman
; APPLICANT: Goddard,Audrey
; APPLICANT: Hillan,Kenneth J.
; APPLICANT: Roth,Iris
; APPLICANT: Wood,William I.
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING BOLEKINE
; FILE REFERENCE: P1192-2 (US)
; CURRENT APPLICATION NUMBER: US/09/816,920
; CURRENT FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US 60/064,249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: US 60/083,336
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: PCT/US99/05028
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 7
; SEQ ID NO 2
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-816-920-2

Query Match 100.0%; Score 587; DB 9; Length 111;
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Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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; Patent No. US20020156006A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
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Query Match 100.0%; Score 587; DB 9; Length 111;
Best Local Similarity 100.0%; Pred. No. 4.9e-58;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
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; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
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; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C27
; CURRENT APPLICATION NUMBER: US/09/978,697
; CURRENT FILING DATE: 2001-10-16
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Query Match 100.0%; Score 587; DB 9; Length 111;
Best Local Similarity 100.0%; Pred. No. 4.9e-58;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
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; Sequence 370, Application US/09978192A
; Patent No. US20020177553A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
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; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
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; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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RESULT 5
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; Sequence 370, Application US/09999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
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;  APPLICANT:  Godowski, Paul J.
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;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
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; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 587; DB 9; Length 111;
Best Local Similarity 100.0%; Pred. No. 4.9e-58;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
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Db         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
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RESULT 6
US-09-978-189-370
; Sequence 370, Application US/09978189
; Publication No. US20030004102A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C7
; CURRENT APPLICATION NUMBER: US/09/978,189
; CURRENT FILING DATE: 2001-10-15
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 587; DB 10; Length 111;
Best Local Similarity 100.0%; Pred. No. 4.9e-58;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
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Db         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
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RESULT 7
US-09-978-608A-370
; Sequence 370, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 370
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-608A-370

Query Match 100.0%; Score 587; DB 10; Length 111;
Best Local Similarity 100.0%; Pred. No. 4.9e-58;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60

Qy         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
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Db         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
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RESULT 8
US-09-978-585A-370
; Sequence 370, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.

```
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C15
;  CURRENT APPLICATION NUMBER: US/09/978,585A
;  CURRENT FILING DATE:  2001-10-16
;  NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 370
;   LENGTH: 111
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-978-585A-370

  Query Match             100.0%;  Score 587;  DB 10;  Length 111;
  Best Local Similarity   100.0%;  Pred. No. 4.9e-58;
  Matches  111;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60
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Db          1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60

Qy         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
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Db         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111


RESULT 9
US-09-978-191A-370
; Sequence 370, Application US/09978191A
; Publication No. US20030050239A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C4
;  CURRENT APPLICATION NUMBER: US/09/978,191A
;  CURRENT FILING DATE:  2001-10-15
;  PRIOR APPLICATION NUMBER: 09/918585
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;  PRIOR APPLICATION NUMBER: 60/064249
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;  PRIOR APPLICATION NUMBER: 60/079664
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Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 10
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; Publication No. US20030050240A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C17
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; Publication No. US20030050241A1
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;  APPLICANT: Ashkenazi, Avi
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;  APPLICANT:  Desnoyers, Luc
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;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 587; DB 10; Length 111;
Best Local Similarity 100.0%; Pred. No. 4.9e-58;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60

Qy         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
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Db         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
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RESULT 12
US-09-999-833A-370
; Sequence 370, Application US/09999833A
; Publication No. US20030054405A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C65
; CURRENT APPLICATION NUMBER: US/09/999,833A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
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Query Match 100.0%; Score 587; DB 10; Length 111;
Best Local Similarity 100.0%; Pred. No. 4.9e-58;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60

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Db         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
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RESULT 13
US-09-981-915A-370
; Sequence 370, Application US/09981915A
; Publication No. US20030054986A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C12
; CURRENT APPLICATION NUMBER: US/09/981,915A
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
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; PRIOR APPLICATION NUMBER: 60/085573
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Query Match 100.0%; Score 587; DB 10; Length 111;
Best Local Similarity 100.0%; Pred. No. 4.9e-58;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60
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Db          1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60

Qy         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
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Db         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
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RESULT 14
US-09-978-824-370
; Sequence 370, Application US/09978824
; Publication No. US20030055216A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C14
; CURRENT APPLICATION NUMBER: US/09/978,824
; CURRENT FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 09/918585
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Query Match 100.0%; Score 587; DB 10; Length 111;
Best Local Similarity 100.0%; Pred. No. 4.9e-58;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Publication No. US20030060406A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C1
; CURRENT APPLICATION NUMBER: US/09/918,585A
; CURRENT FILING DATE: 2001-07-30
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Query Match 100.0%; Score 587; DB 10; Length 111;
Best Local Similarity 100.0%; Pred. No. 4.9e-58;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60
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Qy         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
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Db         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
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Search completed: April 22, 2004, 12:39:35
Job time : 44 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 22, 2004, 12:25:57 ; Search time 55 Seconds
(without alignments)
570.232 Million cell updates/sec

Title: US-09-978-189-370
Perfect score: 587
Sequence: 1 MSLLPRRAPPVSMRLLAAAL.....TKRFIKWYNAWNEKRRVYEE 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	587	100.0	111	2	AAY41739	Aay41739 Human PRO
2	587	100.0	111	2	AAY28290	Aay28290 Tim-1 pro
3	587	100.0	111	3	AAB33423	Aab33423 Human PRO
4	587	100.0	111	3	AAB44295	Aab44295 Human PRO
5	587	100.0	111	4	AAB88478	Aab88478 Human mem
6	587	100.0	111	5	ABG70798	Abg70798 Human Bol
7	587	100.0	111	6	ABO25241	Abo25241 Novel hum
8	587	100.0	111	6	ABU72247	Abu72247 Novel hum
9	587	100.0	111	6	ABB99340	Abb99340 Amino aci
10	587	100.0	111	6	ABU84927	Abu84927 Human sec
11	587	100.0	111	6	ABU61125	Abu61125 Human PRO
12	587	100.0	111	6	ABU80394	Abu80394 Human sec
13	587	100.0	111	6	ADA24909	Ada24909 Novel hum
14	587	100.0	111	6	ABO19696	Abo19696 Novel hum
15	587	100.0	111	6	ADA12570	Ada12570 Human sec
16	587	100.0	111	6	ABO19587	Abo19587 Novel hum
17	587	100.0	111	7	ADB73876	Adb73876 Human PRO
18	587	100.0	111	7	ADB76592	Adb76592 Human PRO
19	587	100.0	111	7	ADC44018	Adc44018 Human sec
20	587	100.0	111	7	ADC61778	Adc61778 Human sec
21	587	100.0	111	7	ADC63742	Adc63742 Human sec
22	587	100.0	111	7	ADC66842	Adc66842 Human sec
23	587	100.0	111	7	ADC68966	Adc68966 Human sec
24	587	100.0	111	7	ADC63026	Adc63026 Human sec
25	587	100.0	111	7	ADC68091	Adc68091 Human sec
26	587	100.0	111	7	ADC41411	Adc41411 Human sec
27	587	100.0	111	7	ADC67466	Adc67466 Human sec
28	587	100.0	111	7	ADC62402	Adc62402 Human sec
29	587	100.0	111	7	ADC42035	Adc42035 Human sec
30	587	100.0	111	7	ADE49404	Ade49404 Human sec
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32	587	100.0	111	7	ADE16572	Ade16572 Human sec
33	587	100.0	111	7	ADD73187	Add73187 Human sec
34	587	100.0	111	7	ADD72545	Add72545 Human sec
35	587	100.0	111	7	ADE17196	Ade17196 Human sec
36	587	100.0	111	8	ADE48704	Ade48704 Human sec
37	587	100.0	111	8	ADE89805	Ade89805 Human sec
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39	582	99.1	111	4	AAG67978	Aag67978 Human mac
40	530	90.3	149	4	AAU31032	Aau31032 Novel hum
41	527	89.8	99	2	AAY31612	Aay31612 Human neo
42	527	89.8	99	5	ABB79372	Abb79372 Human SCY
43	527	89.8	99	6	ABG74456	Abg74456 Human neo
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45	519	88.4	108	4	AAO06902	Aao06902 Human pol

ALIGNMENTS

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ID AAY41739 standard; protein; 111 AA.
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AC AAY41739;
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DT 07-DEC-1999 (first entry)
XX
DE Human PRO273 protein sequence.
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KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW secreted protein; transmembrane protein.
XX
OS Homo sapiens.
XX
PN WO9946281-A2.
XX
PD 16-SEP-1999.
XX
PF 08-MAR-1999; 99WO-US005028.
XX
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PR 11-MAR-1998; 98US-0077632P.
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PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
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PR 01-APR-1998; 98US-0080328P.

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PR 28-MAY-1998; 98US-0087106P.
PR 28-MAY-1998; 98US-0087208P.
PR 30-JUL-1998; 98US-0094651P.
PR 11-SEP-1998; 98US-0100038P.
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PA (GETH) GENENTECH INC.
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PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX
DR WPI; 1999-551358/46.
DR N-PSDB; AAZ34205.
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PT New secreted and transmembrane polypeptides and their polynucleotides,
PT useful for treating blood coagulation disorders, cancers and cellular
PT adhesion disorders.
XX
PS Claim 12; Fig 149; 530pp; English.
XX
CC The present invention describes secreted and transmembrane polypeptides
CC and their polynucleotides. The nucleotide sequences are useful as sources
CC of probes, primers, for chromosome mapping, and for generation of
CC antisense sequences. They can also be used to create transgenic animals.
CC The proteins can be used to treat a variety of diseases and disorders,
CC depending on their function. Diseases that may be treated include blood
CC coagulation disorders, cancers and cellular adhesion disorders. They may
CC also be used to raise antibodies. AAZ33891 to AAZ34338, and AAY41685 to
CC AAY41774 represent polynucleotide and polypeptide sequence given in the
CC exemplification of the present invention
XX
SQ Sequence 111 AA;

Query Match 100.0%; Score 587; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 8.9e-60;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSLLPRRAPPVSMRLLAAALLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60
Db 1 MSLLPRRAPPVSMRLLAAALLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60

Qy 61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
Db 61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111

RESULT 2
AAY28290
ID AAY28290 standard; protein; 111 AA.
XX
AC AAY28290;
XX
DT 28-SEP-1999 (first entry)
XX
DE Tim-1 protein.
XX
KW Chemokine; CXC; Tim-1; inflammation; heart attack; stroke; infection; ss;
KW trauma; radiation; burns; frostbite; corrosive chemical; gene therapy.
XX
OS Homo sapiens.
XX
PN WO9933990-A1.
XX
PD 08-JUL-1999.
XX
PF 14-DEC-1998; 98WO-US026546.
XX
PR 30-DEC-1997; 97US-0068955P.
XX
PA (CHIR) CHIRON CORP.
XX
PI Chen TT, Pot D, Kassam A;
XX
DR WPI; 1999-430244/36.
DR N-PSDB; AAX89708.
XX
PT A new human CXC chemokine, Tim-1, useful for treating inflammation.
XX
PS Claim 1; Page 43; 46pp; English.
XX
CC This is the amino acid sequence for the Tim-1 CXC chemokine. The Tim-1
CC gene can be used to design therapeutic tools for treating inflammation
CC due to stimuli such as heart attacks and stroke, infection, physical
CC trauma, UV or ionizing radiation, burns, frostbite or corrosive
CC chemicals. The Tim-1 gene and subgenomic polynucleotides can be used in
CC gene therapy
XX
SQ Sequence 111 AA;

Query Match 100.0%; Score 587; DB 2; Length 111;

```
  Best Local Similarity   100.0%;  Pred. No. 8.9e-60;
  Matches  111;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60

Qy         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111


RESULT 3
AAB33423
ID   AAB33423 standard; protein; 111 AA.
XX
AC   AAB33423;
XX
DT   29-JAN-2001  (first entry)
XX
DE   Human PRO273 protein UNQ240 SEQ ID NO:46.
XX
KW   Human; immune related disease; diagnosis; antiinflammatory; cardiant;
KW   dermatological; antiarthritic; antirheumatic; immunosuppressive;
KW   haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
KW   antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;
KW   antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
KW   osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
KW   idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
KW   systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
KW   autoimmune thrombocytopaenia; immune-mediated renal disease;
KW   demyelinating disease; hepatobiliary disease; Whipple's disease;
KW   inflammatory bowel disease; gluten-sensitive enteropathy;
KW   autoimmune disease; immune-mediated skin disease; allergic disease;
KW   immunological disease; transplantation associated disease;
KW   graft rejection; graft-versus-host-disease.
XX
OS   Homo sapiens.
XX
PN   WO200053758-A2.
XX
PD   14-SEP-2000.
XX
PF   02-MAR-2000; 2000WO-US005841.
XX
PR   08-MAR-1999;   99WO-US005028.
PR   10-MAR-1999;   99US-0123618P.
PR   12-MAR-1999;   99US-0123957P.
PR   23-MAR-1999;   99US-0125775P.
PR   12-APR-1999;   99US-0128849P.
PR   20-APR-1999;   99WO-US008615.
PR   28-APR-1999;   99US-0131445P.
PR   04-MAY-1999;   99US-0132371P.
PR   14-MAY-1999;   99US-0134287P.
PR   02-JUN-1999;   99WO-US012252.
PR   23-JUN-1999;   99US-0141037P.
PR   20-JUL-1999;   99US-0144758P.
PR   26-JUL-1999;   99US-0145698P.
PR   28-JUL-1999;   99US-0146222P.
PR   01-SEP-1999;   99WO-US020111.
PR   08-SEP-1999;   99WO-US020594.
PR   13-SEP-1999;   99WO-US020944.
PR   15-SEP-1999;   99WO-US021090.
PR   15-SEP-1999;   99WO-US021547.
PR   05-OCT-1999;   99WO-US023089.
PR   29-OCT-1999;   99US-0162506P.
PR   29-NOV-1999;   99WO-US028214.
PR   30-NOV-1999;   99WO-US028313.
PR   30-NOV-1999;   99WO-US028409.
PR   01-DEC-1999;   99WO-US028301.
PR   01-DEC-1999;   99WO-US028634.
PR   02-DEC-1999;   99WO-US028551.
PR   02-DEC-1999;   99WO-US028564.
PR   02-DEC-1999;   99WO-US028565.
PR   16-DEC-1999;   99WO-US030095.
PR   20-DEC-1999;   99WO-US030999.
PR   30-DEC-1999;   99WO-US031274.
PR   05-JAN-2000; 2000WO-US000219.
PR   06-JAN-2000; 2000WO-US000277.
PR   06-JAN-2000; 2000WO-US000376.
PR   11-FEB-2000; 2000WO-US003565.
PR   18-FEB-2000; 2000WO-US004341.
PR   18-FEB-2000; 2000WO-US004342.
PR   22-FEB-2000; 2000WO-US004414.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Goddard A,  Gurney AL,  Hebert C,  Henzel W;
PI   Kabakoff RC,  Lu Y,  Pan J,  Pennica D,  Shelton DL,  Smith V;
PI   Stewart TA,  Tumas D,  Watanabe CK,  Wood WI,  Yan M;
XX
DR   WPI; 2000-572271/53.
DR   N-PSDB; AAC58588.
XX
PT   Sixty four PRO polypeptides, useful in the diagnosis and treatment of
PT   immune related disorders, e.g. systemic lupus erythematosis, rheumatoid
PT   arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
XX
PS   Claim 33; Fig 20; 309pp; English.
XX
CC   The present invention describes sixty four human PRO proteins which can
CC   be used in the treatment of immune related diseases. The human PRO
CC   proteins, anti-PRO antibodies, agonists and antagonists are useful for
CC   treating and diagnosing immune related disorders. The disorders are
CC   selected from systemic lupus erythematosus, rheumatoid arthritis,
CC   osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
CC   systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC   syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
CC   anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
CC   immune-mediated renal disease, demyelinating diseases of the central and
CC   peripheral nervous systems, hepatobiliary diseases, inflammatory bowel
CC   disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune
CC   or immune-mediated skin diseases, allergic diseases, immunological
CC   diseases of the lung, and transplantation associated diseases including
CC   graft rejection and graft-versus-host-disease. AAC58397 to AAC58578
CC   represent PCR primers and hybridisation probes used in the isolation of
CC   human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477
CC   represent human PRO polynucleotide and protein sequences given in the
CC   exemplification of the present invention
XX
SQ   Sequence 111 AA;

  Query Match             100.0%;  Score 587;  DB 3;  Length 111;
  Best Local Similarity   100.0%;  Pred. No. 8.9e-60;
  Matches  111;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60

Qy         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111


RESULT 4
AAB44295
ID   AAB44295 standard; protein; 111 AA.
XX
AC   AAB44295;
XX
DT   08-FEB-2001  (first entry)
XX
DE   Human PRO273 (UNQ240) protein sequence SEQ ID NO:370.
XX
KW   Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;
```

KW expressed sequence tag; detection; cancer.
XX
OS *Homo sapiens*.
XX
PN WO200053756-A2.
XX
PD 14-SEP-2000.
XX
PF 18-FEB-2000; 2000WO-US004341.
XX
PR 08-MAR-1999; 99WO-US005028.
PR 12-MAR-1999; 99US-0123957P.
PR 29-MAR-1999; 99US-0126773P.
PR 21-APR-1999; 99US-0130232P.
PR 28-APR-1999; 99US-0131445P.
PR 14-MAY-1999; 99US-0134287P.
PR 23-JUN-1999; 99US-0141037P.
PR 26-JUL-1999; 99US-0145698P.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR WPI; 2000-611443/58.
DR N-PSDB; AAC78551.
XX
PT Novel PRO polypeptides and polynucleotides used in detection methods, to
PT target bioactive molecules to specific cells, and to modulate cellular
PT activities.
XX
PS Claim 12; Fig 149; 636pp; English.
XX
CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence
CC tag) sequences which encode secreted or transmembrane PRO polypeptides.
CC The PRO polynucleotides and polypeptides have cytostatic activity. The
CC polynucleotides and polypeptides can be used for detecting the presence
CC of PRO polypeptides in samples, for linking bioactive molecules to cells
CC and for modulating biological activities of cells, using the polypeptides
CC for specific targeting. The polypeptide targeting can be used to kill the
CC target cells, e.g. for the treatment of cancers. The polypeptide pairs
CC provide specific targeting of bioactive molecules to cells. AAC78600 to
CC AAC78987 represent PCR primers and probes used in the isolation of the
CC PRO polynucleotide sequences
XX
SQ Sequence 111 AA;

Query Match 100.0%; Score 587; DB 3; Length 111;
Best Local Similarity 100.0%; Pred. No. 8.9e-60;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60

Qy         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
```

RESULT 5
AAB88478
ID AAB88478 standard; protein; 111 AA.
XX
AC AAB88478;
XX
DT 23-MAY-2001 (first entry)
XX
DE *Human membrane or secretory protein clone PSEC0212.*
XX
KW Human; secretory protein; membrane protein; vaccine; gene therapy;
KW rheumatoid arthritis; diabetes.
XX
OS Homo sapiens.
XX
PN EP1067182-A2.
XX
PD 10-JAN-2001.
XX
PF 07-JUL-2000; 2000EP-00114090.
XX
PR 08-JUL-1999; 99JP-00194179.
PR 11-JAN-2000; 2000JP-00118775.
PR 02-MAY-2000; 2000JP-00183766.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
XX
DR WPI; 2001-093989/11.
DR N-PSDB; AAF93905.
XX
PT Nucleic acids encoding secretory proteins/membrane proteins, useful in
PT gene therapy or as candidate target molecules in drug development.
XX
PS Claim 1; SEQ ID NO 324; 609pp + Sequence Listing; English.
XX
CC This invention relates to nucleic acid sequences AAF93744 - AAF93916
CC which encode human secretory or membrane proteins represented by AAB88317
CC - AAB88419. Included in the invention are primers AAF93917 - AAF94295 and
CC AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the
CC invention. The invention also includes methods for the production of
CC antibodies directed against the proteins, and cDNA sequences, which can
CC be used in vaccines. The polynucleotide sequences can be used in gene
CC therapy. The polynucleotide sequences and the proteins they encode may be
CC used in the prevention, treatment and diagnosis of diseases associated
CC with inappropriate secretory protein/membrane protein expression. The
CC nucleic acids and complementary sequences may also be used as DNA probes
CC in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect
CC and quantitate the presence of similar nucleic acid sequences in samples.
CC They may also be used to study the expression and function of secretory
CC proteins/membrane polypeptides and their role in metabolism. The
CC polypeptides may be used as antigens in the production of antibodies
CC against them and in assays to identify modulators (agonists and
CC antagonists) of expression and activity. The antibodies and antagonists
CC may also be used as therapeutic agents to down regulate expression and
CC activity. The antibodies may also be used as diagnostic agents for
CC detecting the presence of the polypeptides in samples (e.g. by enzyme
CC linked immunosorbant assay (ELISA). Examples of diseases which may be
CC treated include rheumatoid arthritis and diabetes
XX
SQ Sequence 111 AA;

Query Match 100.0%; Score 587; DB 4; Length 111;
Best Local Similarity 100.0%; Pred. No. 8.9e-60;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60

Qy         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
              |||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111

RESULT 6
ABG70798
ID   ABG70798 standard; protein; 111 AA.
XX
AC   ABG70798;
XX
DT   16-DEC-2002  (first entry)
XX
DE   Human Bolekine protein.
XX
KW   Human; Bolekine; leukocyte; immune response; chemokine;
KW   leukocyte trafficking; adhesion; endothelial cell; chemoattractant;
KW   proliferation; activation; systemic lupus erythematosus; arthritis;
KW   angiogenesis; systemic sclerosis; autoimmune haemolytic anaemia;
KW   thyroiditis; diabetes mellitus; renal disease; demyelinating disease;
KW   nervous system; polyneuropathy; hepatitis; primary biliary cirrhosis;
KW   inflammatory bowel disease; autoimmune skin disease; alopecia; psoriasis;
KW   allergy; asthma; atopic dermatitis; food hypersensitivity; lung disease;
KW   stroke; encephalitis; multiple sclerosis; agonist; antagonist;
KW   T-lymphocyte; mononuclear cell; eosinophil; polymorphonuclear neutrophil;
KW   PMN; pluripotent cell; neuronal cell; MAP2; transgenic; therapeutic;
KW   gene therapy; tumour; neovascularisation.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .34
FT                   /label= Signal_peptide
FT   Protein         35. .111
FT                   /label= Mature_Bolekine
FT   Modified-site   80. .85
FT                   /note= "N-myristoylation site"
XX
PN   US2002119118-A1.
XX
PD   29-AUG-2002.
XX
PF   22-MAR-2001; 2001US-00816920.
XX
PR   03-NOV-1997;   97US-0064249P.
PR   27-APR-1998;   98US-0083336P.
PR   08-MAR-1999;   99WO-US005028.
PR   18-FEB-2000; 2000WO-US004341.
PR   02-MAR-2000; 2000WO-US005841.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Fong S,  Goddard A,  Hillan KJ,  Roth I,  Wood WI;
XX
DR   WPI; 2002-740172/80.
DR   N-PSDB; ABS55212.
XX
PT   Novel Bolekine polypeptide useful for identifying agonist and antagonist
PT   of the polypeptide, and for treating immune related disorder, e.g.
PT   systemic lupus erythematosus and rheumatoid arthritis in a mammal.
XX
PS   Claim 15; Fig 2; 63pp; English.
XX
CC   The invention discloses a human Bolekine polypeptide, or its fragment.
CC   Leukocytes play a important role in the immune response and the processes
CC   by which these cells move to their appropriate destination is critical.
CC   Chemokines are involved in leukocyte trafficking by mediating the
CC   expression of adhesion molecules on endothelial cells, producing
CC   chemoattractants, stimulate proliferation and regulate activation of
CC   specific cell types. The polynucleotide, polypeptide and antibodies
CC   raised against the polypeptide are useful for treating an immune related
CC   disorder in a mammal, such as systemic lupus erythematosus, arthritis,
CC   angiogenesis, systemic sclerosis, autoimmune haemolytic anaemia,
CC   thyroiditis, diabetes mellitus, renal disease, demyelinating disease of
CC   the central or peripheral nervous system, polyneuropathy, hepatitis,
CC   primary biliary cirrhosis, inflammatory bowel disease, an autoimmune or
CC   immune-mediated skin disease, alopecia, psoriasis, allergic disease,
CC   asthma, atopic dermatitis, food hypersensitivity, immunologic disease of
CC   the lung, stroke, encephalitis and multiple sclerosis. The polypeptides
CC   and polynucleotides are also useful for identifying a compound (agonist
CC   or antagonist) that inhibits the expression of activity of Bolekine, for
CC   diagnosing an immune related disease in a mammal, for modulating the
CC   proliferation of T-lymphocytes for enhancing the infiltration of
CC   inflammatory cells (such as mononuclear cells, eosinophils and
CC   polymorphonuclear neutrophils (PMNs)) into a tissue of a mammal and for
CC   inducing the differentiation of pluripotent cells into neuronal cells in
CC   a mammal, where the cells differentiate to a state such that neuronal
CC   markers (e.g. MAP2) are detected. The polynucleotides are also useful for
CC   generating transgenic or knock out animals which can be used in the
CC   development and screening of therapeutically useful agents, in gene
CC   therapy, chromosome markers and diagnostically for tissue typing and for
CC   treating tumours by inhibiting the neovascularisation. The sequence
CC   presented is the human Bolekine protein
XX
SQ   Sequence 111 AA;

  Query Match             100.0%;  Score 587;  DB 5;  Length 111;
  Best Local Similarity   100.0%;  Pred. No. 8.9e-60;
  Matches  111;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60

Qy         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111


RESULT 7
ABO25241
ID   ABO25241 standard; protein; 111 AA.
XX
AC   ABO25241;
XX
DT   09-SEP-2003  (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO273.
XX
KW   Human; secreted and transmembrane protein; PRO; virucide; gene therapy;
KW   cell death; growth induction cascade; blood coagulation cascade;
KW   viral infection.
XX
OS   Homo sapiens.
XX
PN   US2003050239-A1.
XX
PD   13-MAR-2003.
XX
PF   15-OCT-2001; 2001US-00978191.
XX
PR   17-OCT-1997;   97US-0062250P.
PR   03-NOV-1997;   97US-0064249P.
PR   13-NOV-1997;   97US-0065311P.
PR   21-NOV-1997;   97US-0066364P.
PR   10-MAR-1998;   98US-0077450P.
PR   11-MAR-1998;   98US-0077632P.
PR   11-MAR-1998;   98US-0077641P.
PR   11-MAR-1998;   98US-0077649P.
PR   12-MAR-1998;   98US-0077791P.
PR   13-MAR-1998;   98US-0078004P.
PR   17-MAR-1998;   98US-00040220.
PR   20-MAR-1998;   98US-0078886P.
PR   20-MAR-1998;   98US-0078910P.
PR   20-MAR-1998;   98US-0078936P.
PR   20-MAR-1998;   98US-0078939P.
PR   25-MAR-1998;   98US-0079294P.
PR   26-MAR-1998;   98US-0079656P.
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PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 31-MAR-1998; 98US-0080105P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080165P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080328P.
PR 01-APR-1998; 98US-0080333P.
PR 01-APR-1998; 98US-0080334P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 08-APR-1998; 98US-0081071P.
PR 09-APR-1998; 98US-0081195P.
PR 09-APR-1998; 98US-0081203P.
PR 09-APR-1998; 98US-0081229P.
PR 15-APR-1998; 98US-0081817P.
PR 15-APR-1998; 98US-0081819P.
PR 15-APR-1998; 98US-0081838P.
PR 15-APR-1998; 98US-0081952P.
PR 15-APR-1998; 98US-0081955P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082700P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
PR 22-APR-1998; 98US-0082804P.
PR 23-APR-1998; 98US-0082796P.
PR 27-APR-1998; 98US-0083336P.
PR 28-APR-1998; 98US-0083322P.
PR 29-APR-1998; 98US-0083392P.
PR 29-APR-1998; 98US-0083495P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083499P.
PR 29-APR-1998; 98US-0083500P.
PR 29-APR-1998; 98US-0083545P.
PR 29-APR-1998; 98US-0083554P.
PR 29-APR-1998; 98US-0083558P.
PR 29-APR-1998; 98US-0083559P.
PR 30-APR-1998; 98US-0083742P.
PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 06-MAY-1998; 98US-0084441P.
PR 07-MAY-1998; 98US-0084598P.
PR 07-MAY-1998; 98US-0084600P.
PR 07-MAY-1998; 98US-0084627P.
PR 07-MAY-1998; 98US-0084637P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
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PR 13-MAY-1998; 98US-0085323P.
PR 13-MAY-1998; 98US-0085338P.
PR 13-MAY-1998; 98US-0085339P.
PR 15-MAY-1998; 98US-0085573P.
PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085689P.
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PR 15-MAY-1998; 98US-0085700P.
PR 15-MAY-1998; 98US-0085704P.
PR 18-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086392P.
PR 22-MAY-1998; 98US-0086414P.
PR 22-MAY-1998; 98US-0086430P.
PR 22-MAY-1998; 98US-0086486P.
PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087106P.
PR 28-MAY-1998; 98US-0087208P.
PR 26-JUN-1998; 98US-00105413.
PR 26-JUN-1998; 98US-0090863P.
PR 26-JUN-1998; 98US-0091010P.
PR 01-JUL-1998; 98US-0091359P.
PR 30-JUL-1998; 98US-0094651P.
PR 11-SEP-1998; 98US-0100038P.
PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98WO-US021141.
PR 02-NOV-1998; 98US-00184216.
PR 06-NOV-1998; 98US-00187368.
PR 20-NOV-1998; 98US-0109304P.
PR 20-NOV-1998; 98WO-US024855.
PR 07-DEC-1998; 98US-00202054.
PR 22-DEC-1998; 98US-00218517.
PR 22-DEC-1998; 98US-0113296P.
PR 23-DEC-1998; 98US-0113621P.
PR 05-JAN-1999; 99WO-US000106.
PR 05-MAR-1999; 99US-00254465.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99US-00265686.
PR 10-MAR-1999; 99WO-US005190.
PR 12-MAR-1999; 99US-00267213.
PR 12-MAR-1999; 99US-0123957P.
PR 29-MAR-1999; 99US-0126773P.
PR 12-APR-1999; 99US-00284291.
PR 21-APR-1999; 99US-0130232P.
PR 26-APR-1999; 99US-0131022P.
PR 28-APR-1999; 99US-0131445P.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99US-0134287P.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 16-JUN-1999; 99US-0139557P.
PR 23-JUN-1999; 99US-0141037P.
PR 07-JUL-1999; 99US-0142680P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380142.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000US-00709238.
PR 27-NOV-2000; 2000US-00723749.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 22-MAR-2001; 2001US-00816920.
PR 22-MAR-2001; 2001WO-US009552.

PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;

Query Match 100.0%; Score 587; DB 6; Length 111;
Best Local Similarity 100.0%; Pred. No. 8.9e-60;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60
Db 1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60

Qy 61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
Db 61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111

RESULT 8
ABU72247
ID ABU72247 standard; protein; 111 AA.
XX
AC ABU72247;
XX
DT 16-JUN-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO273.
XX
KW Human; secreted and transmembrane protein; PRO; antiinflammatory;
KW antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;
KW antidiabetic; gene therapy; inflammatory disease; organ failure;
KW atherosclerosis; cardiac injury; infertility; birth defect;
KW premature aging; AIDS; cancer; diabetic complication; chromosome mapping;
KW gene mapping; pharmaceutical; diagnostic; biosensor; bioreactor;
KW tissue typing.
XX
OS Homo sapiens.
XX
PN US2002192706-A1.
XX
PD 19-DEC-2002.
XX
PF 24-OCT-2001; 2001US-00999832.
XX
PR 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-00040220.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079294P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 31-MAR-1998; 98US-0080105P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080165P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080328P.
PR 01-APR-1998; 98US-0080333P.
PR 01-APR-1998; 98US-0080334P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 08-APR-1998; 98US-0081071P.
PR 09-APR-1998; 98US-0081195P.
PR 09-APR-1998; 98US-0081203P.
PR 09-APR-1998; 98US-0081229P.
PR 15-APR-1998; 98US-0081817P.
PR 15-APR-1998; 98US-0081819P.
PR 15-APR-1998; 98US-0081838P.
PR 15-APR-1998; 98US-0081952P.
PR 15-APR-1998; 98US-0081955P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082700P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
PR 22-APR-1998; 98US-0082804P.
PR 23-APR-1998; 98US-0082796P.
PR 07-OCT-1998; 98WO-US021141.
PR 20-NOV-1998; 98WO-US024855.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001WO-US009552.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
XX

PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR WPI; 2003-328860/31.
DR N-PSDB; ACA63773.
XX
PT New secreted and transmembrane nucleic acids and polypeptides, designated
PT as PRO, useful for treating inflammation, organ failure, atherosclerosis,
PT cardiac injury, infertility, birth defects, premature aging, AIDS, or
PT cancer.
XX
PS Claim 12; Fig 149; 453pp; English.
XX
CC The invention describes an isolated nucleic acid (I) comprising, or which
CC is at least 80 % sequence identity to, or the full-length coding sequence
CC of, any of 118 300-2100 nucleotide sequences, which encodes its
CC corresponding PRO polypeptide selected from 118 100-700 amino acid
CC sequences, all given in the specification. The nucleic acids and
CC polypeptides are useful for treating inflammatory diseases, organ
CC failure, atherosclerosis, cardiac injury, infertility, birth defects,
CC premature aging, AIDS, cancer, or diabetic complications. The nucleic
CC acids are useful as hybridisation probes, in chromosome and gene mapping,
CC and in generating antisense RNA or DNA. The polypeptides are useful as
CC pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful
CC in tissue typing. This is the amino acid sequence of a novel human
CC secreted and transmembrane PRO polypeptide
XX
SQ Sequence 111 AA;

Query Match 100.0%; Score 587; DB 6; Length 111;
Best Local Similarity 100.0%; Pred. No. 8.9e-60;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60
Db 1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60

Qy 61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
Db 61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111

RESULT 9
ABB99340
ID ABB99340 standard; protein; 111 AA.
XX
AC ABB99340;
XX
DT 29-JAN-2003 (first entry)
XX
DE Amino acid sequence of Human Bolekine.
XX
KW Human; Bolekine; T-lymphocyte proliferation; immune related disorder;
KW systemic lupus erythematosis; rheumatoid arthritis; osteoarthritis;
KW juvenile chronic arthritis; spondyloarthropathy; systemic sclerosis;
KW idiopathic inflammatory myopathy; Sjogren's syndrome;
KW systemic vasculitis; sarcoidosis; autoimmune haemolytic anaemia;
KW autoimmune thromobocytopaenia; thyroiditis; diabetes mellitus;
KW immune-mediated renal disease; demyelinating disease;
KW idiopathic demyelinating polyneuropathy; Guillen-Barre syndrome;
KW chronic inflammatory demyelinating polyneuropathy; hepatobiliary disease;
KW hepatitis; primary biliary cirrhosis; granulomatous hepatitis;
KW sclerosing cholangitis; inflammatory bowel disease;
KW gluten-sensitive enteropathy; Whipple's disease; skin disease;
KW erythema multiforme; contact dermatitis; psoriasis; allergy; asthma;
KW allergic rhinitis; atopic dermatitis; food hypersensitivity; urticaria;
KW eosinophilic pneumonia; idiopathic pulmonary fibrosis;
KW hypersensitivity pneumonitis; graft rejection; graft-versus-host disease;
KW gene therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1. .34
FT /note= "signal peptide"
FT Modified-site 80. .85
FT /note= "N-myristoylation site"
XX
PN WO200277028-A1.
XX
PD 03-OCT-2002.
XX
PF 22-MAR-2001; 2001WO-US009552.
XX
PR 22-MAR-2001; 2001WO-US009552.
XX
PA (GETH) GENENTECH INC.
XX
PI Fong S, Goddard A, Hillan KJ, Roth I, Wood WI;
XX
DR WPI; 2003-018887/01.
DR N-PSDB; ABV72423.
XX
PT New Bolekine polypeptides and encoding nucleic acids, useful for treating
PT an immune related disorder such as systemic lupus erythematosis,
PT rheumatoid arthritis, psoriasis, asthma, allergic rhinitis and atopic
PT dermatitis.
XX
PS Claim 15; Fig 2; 96pp; English.
XX
CC The present sequence represents a human Bolekine polypeptide. Bolekine
CC polypeptides are active stimulators of the proliferation of T-
CC lymphocytes. Bolekine polypeptides and polynucleotides are useful for
CC treating an immune related disorder e.g. systemic lupus erythematosis,
CC rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, a
CC spondyloarthropathy, systemic sclerosis, an idiopathic inflammatory
CC myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis,
CC autoimmune haemolytic anaemia, autoimmune thromobocytopaenia,
CC thyroiditis, diabetes mellitus, immune-mediated renal disease, a
CC demyelinating disease of the central or peripheral nervous system,
CC idiopathic demyelinating polyneuropathy, Guillen-Barre syndrome, a
CC chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
CC disease, infectious or autoimmune chronic active hepatitis, primary
CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
CC disease, asthma, allergic rhinitis, atopic dermatitis, food
CC hypersensitivity, urticaria, an immunologic disease of the lung,
CC eosinophilic pneumonias, idiopathic pulmonary fibrosis, hypersensitivity
CC pneumonitis, a transplantation associated disease, graft rejection or
CC graft-versus-host disease. The Bolekine polypeptides and encoding nucleic
CC acid molecules can also be used as hybridization probes, for generation
CC of transgenic animal, gene therapy, as molecular weight markers,
CC chromosome identification and tissue typing
XX
SQ Sequence 111 AA;

Query Match 100.0%; Score 587; DB 6; Length 111;
Best Local Similarity 100.0%; Pred. No. 8.9e-60;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60
Db 1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60

Qy 61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
Db 61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111

RESULT 10
ABU84927
ID ABU84927 standard; protein; 111 AA.
XX
AC ABU84927;
XX
DT 12-AUG-2003 (first entry)
XX
DE Human secreted and transmembrane PRO polypeptide #3.
XX
KW Human; thrombolytic agent; interferon; interleukin; cytokine;
KW erythropoietin; colony stimulating factor; cancer; colorectal carcinoma;
KW apoptosis related condition; AIDS; amyotrophic lateral sclerosis;
KW inflammatory disease; asthma; atherosclerosis; neurodegenerative disease;
KW gastrointestinal disorder; Alzheimer's disease; Parkinson's disease;
KW hypertension; myocardial ischaemia; kidney disease; carcinogenesis;
KW glomerulonephritis; lung disease; pulmonary hypertension; preeclampsia;
KW bronchial asthma; gastric ulcer; renal failure; cardiovascular disease;
KW inflammatory bowel disease; reproductive disorder; premature labour.
XX
OS Homo sapiens.
XX
PN US2002177553-A1.
XX
PD 28-NOV-2002.
XX
PF 15-OCT-2001; 2001US-00978192.
XX
PR 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-00040220.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079294P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 26-JUN-1998; 98US-00105413.
PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98WO-US021141.
PR 02-NOV-1998; 98US-00184216.
PR 06-NOV-1998; 98US-00187368.
PR 20-NOV-1998; 98WO-US024855.
PR 07-DEC-1998; 98US-00202054.
PR 22-DEC-1998; 98US-00218517.
PR 05-JAN-1999; 99WO-US000106.
PR 05-MAR-1999; 99US-00254465.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99US-00265686.
PR 10-MAR-1999; 99WO-US005190.
PR 12-MAR-1999; 99US-00267213.
PR 12-APR-1999; 99US-00284291.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380142.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000US-00709238.
PR 27-NOV-2000; 2000US-00723749.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 22-MAR-2001; 2001US-00816920.
PR 22-MAR-2001; 2001WO-US009552.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
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PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
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PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR WPI; 2003-328499/31.
DR N-PSDB; ACA71937.
XX
PT New isolated PRO polypeptides e.g. PRO213, PRO274 and PRO300, for use as
PT pharmaceuticals, diagnostics, biosensors and bioreactors, for identifying
PT modulators of receptor-ligand interactions.
XX
PS Claim 12; SEQ ID NO 370; 55pp; English.
XX
CC The invention relates to an isolated secreted and transmembrane
CC polypeptide, designated as PRO polypeptide. The PRO polypeptide is useful
CC in PRO polypeptide detection methods. The PRO polypeptide is useful for
CC linking a bioactive molecule to a cell. The PRO polypeptide or an
CC antibody against it is useful for modulating a biological activity of a
CC cell. The PRO polypeptide is useful in industrial applications including
CC pharmaceuticals, diagnostics, biosensors and bioreactors. The PRO
CC polypeptide is also useful as a thrombolytic agent, interferon,
CC interleukin, erythropoietin, colony stimulating factor and other
CC cytokines. The PRO polypeptide is useful for treating disease such as
CC cancer e.g. colorectal carcinoma; apoptosis related conditions e.g. AIDS,
CC amyotrophic lateral sclerosis; inflammatory disease e.g. asthma,

```
CC   atherosclerosis; neurodegenerative disease e.g. Alzheimer's disease,
CC   Parkinson's disease; cardiovascular disease e.g. hypertension and
CC   myocardial ischaemia; kidney disease e.g. renal failure and
CC   glomerulonephritis; lung disease e.g. pulmonary hypertension, bronchial
CC   asthma; gastrointestinal disorders e.g. gastric ulcer and inflammatory
CC   bowel disease; reproductive disorders e.g. premature labour and
CC   preeclampsia; carcinogenesis. The present sequence represents the amino
CC   acid sequence of a PRO polypeptide of the invention. Note: The sequence
CC   data for this patent did not form part of the printed specification but
CC   was obtained in electronic format directly from USPTO at
CC   seqdata.uspto.gov/sequence.html?DocID=20020177553
XX
SQ   Sequence 111 AA;

  Query Match           100.0%;  Score 587;  DB 6;  Length 111;
  Best Local Similarity  100.0%;  Pred. No. 8.9e-60;
  Matches  111;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60

Qy         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111


RESULT 11
ABU61125
ID   ABU61125 standard; protein; 111 AA.
XX
AC   ABU61125;
XX
DT   08-MAY-2003  (first entry)
XX
DE   Human PRO273 polypeptide.
XX
KW   Human; PRO polypeptide; secreted and transmembrane protein;
KW   immune disorder; diabetes; hyper-insulinaemia; hypo-insulinaemia;
KW   cardiac insufficiency; nervous system disorder; kidney disorder;
KW   bone disorder; cartilage disorder; arthritis; tumour; wound healing;
KW   genetic disorder; cytostatic; antidiabetic; antiinflammatory;
KW   antiarthritic; anti-tumour; vulnerary; antianaemic; dermatological;
KW   cardiant.
XX
OS   Homo sapiens.
XX
PN   US2002169284-A1.
XX
PD   14-NOV-2002.
XX
PF   16-OCT-2001; 2001US-00978697.
XX
PR   26-MAY-1981;   81US-00267213.
PR   17-OCT-1997;   97US-0062250P.
PR   03-NOV-1997;   97US-0064249P.
PR   13-NOV-1997;   97US-0065311P.
PR   21-NOV-1997;   97US-0066364P.
PR   10-MAR-1998;   98US-0077450P.
PR   11-MAR-1998;   98US-0077632P.
PR   11-MAR-1998;   98US-0077641P.
PR   11-MAR-1998;   98US-0077649P.
PR   12-MAR-1998;   98US-0077791P.
PR   13-MAR-1998;   98US-0078004P.
PR   17-MAR-1998;   98US-00040220.
PR   20-MAR-1998;   98US-0078886P.
PR   20-MAR-1998;   98US-0078910P.
PR   20-MAR-1998;   98US-0078936P.
PR   20-MAR-1998;   98US-0078939P.
PR   25-MAR-1998;   98US-0079294P.
PR   26-MAR-1998;   98US-0079656P.
PR   27-MAR-1998;   98US-0079663P.
PR   27-MAR-1998;   98US-0079664P.
PR   27-MAR-1998;   98US-0079689P.
PR   27-MAR-1998;   98US-0079728P.
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PR   30-MAR-1998;   98US-0079920P.
PR   30-MAR-1998;   98US-0079923P.
PR   26-JUN-1998;   98US-00105413.
PR   07-OCT-1998;   98US-00168978.
PR   07-OCT-1998;   98WO-US021141.
PR   02-NOV-1998;   98US-00184216.
PR   06-NOV-1998;   98US-00187368.
PR   20-NOV-1998;   98WO-US024855.
PR   07-DEC-1998;   98US-00202054.
PR   22-DEC-1998;   98US-00218517.
PR   05-JAN-1999;   99WO-US000106.
PR   05-MAR-1999;   99US-00254465.
PR   08-MAR-1999;   99WO-US005028.
PR   10-MAR-1999;   99US-00265686.
PR   10-MAR-1999;   99WO-US005190.
PR   12-APR-1999;   99US-00284291.
PR   14-MAY-1999;   99US-00311832.
PR   14-MAY-1999;   99WO-US010733.
PR   02-JUN-1999;   99WO-US012252.
PR   25-AUG-1999;   99US-00380137.
PR   25-AUG-1999;   99US-00380138.
PR   25-AUG-1999;   99US-00380142.
PR   30-NOV-1999;   99WO-US028313.
PR   02-DEC-1999;   99WO-US028551.
PR   02-DEC-1999;   99WO-US028565.
PR   16-DEC-1999;   99WO-US030095.
PR   30-DEC-1999;   99WO-US031243.
PR   30-DEC-1999;   99WO-US031274.
PR   05-JAN-2000; 2000WO-US000219.
PR   06-JAN-2000; 2000WO-US000277.
PR   06-JAN-2000; 2000WO-US000376.
PR   11-FEB-2000; 2000WO-US003565.
PR   18-FEB-2000; 2000WO-US004341.
PR   24-FEB-2000; 2000WO-US005004.
PR   02-MAR-2000; 2000WO-US005841.
PR   10-MAR-2000; 2000WO-US006319.
PR   21-MAR-2000; 2000WO-US007532.
PR   30-MAR-2000; 2000WO-US008439.
PR   17-MAY-2000; 2000WO-US013705.
PR   22-MAY-2000; 2000WO-US014042.
PR   30-MAY-2000; 2000WO-US014941.
PR   02-JUN-2000; 2000WO-US015264.
PR   28-JUL-2000; 2000WO-US020710.
PR   24-AUG-2000; 2000WO-US023328.
PR   08-NOV-2000; 2000US-00709238.
PR   27-NOV-2000; 2000US-00723749.
PR   01-DEC-2000; 2000WO-US032678.
PR   20-DEC-2000; 2000US-00747259.
PR   20-DEC-2000; 2000WO-US034956.
PR   28-FEB-2001; 2001WO-US006520.
PR   22-MAR-2001; 2001US-00816744.
PR   22-MAR-2001; 2001US-00816920.
PR   22-MAR-2001; 2001WO-US009552.
PR   10-MAY-2001; 2001US-00854208.
PR   10-MAY-2001; 2001US-00854280.
PR   25-MAY-2001; 2001WO-US017092.
PR   01-JUN-2001; 2001US-00872035.
PR   01-JUN-2001; 2001WO-US017800.
PR   05-JUN-2001; 2001US-00874503.
PR   14-JUN-2001; 2001US-00882636.
PR   19-JUN-2001; 2001US-00886342.
PR   20-JUN-2001; 2001WO-US019692.
PR   29-JUN-2001; 2001WO-US021066.
PR   09-JUL-2001; 2001WO-US021735.
PR   30-JUL-2001; 2001US-00918585.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi A,  Baker KP,  Botstein D,  Desnoyers L,  Eaton D;
PI   Ferrara N,  Filvaroff E,  Fong S,  Gao W,  Gerber H,  Gerritsen ME;
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PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR WPI; 2003-288163/28.
DR N-PSDB; ABX92577.
XX
PT Novel secreted and transmembrane polypeptides and polynucleotides
PT encoding them useful for treating cancer, kidney diseases, bone,
PT cartilage disorders and immune deficiencies.
XX
PS Claim 12; Fig 149; 459pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for linking
CC bioactive molecules to cells expressing PRO polypeptides, for modulating
CC biological activities of cells expressing PRO polypeptides, and for for
CC identifying agonists or antagonists. The bioactive molecule maybe a
CC toxin, radiolabel or antibody, and causes apoptosis or death of the cell.
CC The PRO polypeptides are useful for treating immune disorders, diabetes
CC or hyper- or hypo-insulinaemia, cardiac insufficiency, nervous system
CC disorders, kidney disorders, bone and cartilage disorders or arthritis,
CC tumours, and wound healing. The polynucleotide sequences encoding PRO
CC polypeptides are useful as hybridisation probes, in chromosome and gene
CC mapping, in the generation of antisense RNA and DNA, in the preparation
CC of PRO polypeptides, for generating transgenic animals or knockout
CC animals, for the genetic analysis of individuals with genetic disorders,
CC and in gene therapy. ABU61071-ABU61164 represent the human PRO
CC polypeptides of the invention. Note: The sequence data for this patent
CC was obtained in electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/psipsDIDEntry.html
XX
SQ Sequence 111 AA;

Query Match 100.0%; Score 587; DB 6; Length 111;
Best Local Similarity 100.0%; Pred. No. 8.9e-60;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60

Qy         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
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RESULT 12
ABU80394
ID ABU80394 standard; protein; 111 AA.
XX
AC ABU80394;
XX
DT 24-JUN-2003 (first entry)
XX
DE Human secreted/transmembrane protein PRO273.
XX
KW Human; secreted protein; transmembrane protein; PRO; malignancy; cancer;
KW ovarian cancer; colorectal cancer; sarcoma; leukaemia; lymphoma;
KW inflammatory disease; necrosis; atherosclerosis; infertility;
KW premature aging; psoriasis; inflammatory disease; renal disease;
KW arthritis; immune-mediated alopecia; stroke; encephalitis; hepatitis;
KW multiple sclerosis; gene therapy.
XX
OS Homo sapiens.
XX
PN US2003004102-A1.
XX
PD 02-JAN-2003.
XX
PF 15-OCT-2001; 2001US-00978189.

XX
PR 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-00040220.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079294P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 26-JUN-1998; 98US-00105413.
PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98WO-US021141.
PR 02-NOV-1998; 98US-00184216.
PR 06-NOV-1998; 98US-00187368.
PR 20-NOV-1998; 98WO-US024855.
PR 07-DEC-1998; 98US-00202054.
PR 22-DEC-1998; 98US-00218517.
PR 05-JAN-1999; 99WO-US000106.
PR 05-MAR-1999; 99US-00254465.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99US-00265686.
PR 10-MAR-1999; 99WO-US005190.
PR 12-MAR-1999; 99US-00267213.
PR 12-APR-1999; 99US-00284291.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380142.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030873.
PR 27-NOV-2000; 2000US-00723749.
PR 01-DEC-2000; 2000WO-US032678.

PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 22-MAR-2001; 2001US-00816920.
PR 22-MAR-2001; 2001WO-US009552.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR WPI; 2003-341189/32.
DR N-PSDB; ACA66318.
XX
PT New genes and secreted and transmembrane polypeptides (e.g. PRO337 or
PT PRO1559), useful for treating or diagnosing e.g. cancers,
PT atherosclerosis, infertility, stroke, encephalitis, hepatitis or multiple
PT sclerosis in mammals.
XX
PS Claim 12; Fig 149; 460pp; English.
XX
CC The invention relates to a new isolated nucleic acid molecule comprises a
CC sequence with at least 80% identity to: (a) a nucleotide encoding any of
CC 94 PRO polypeptides whose sequences are fully defined in the
CC specification; or (b) any of 94 nucleotide sequences fully defined in the
CC specification; or the full length coding sequence of any these 94
CC nucleotide sequences. Also included are an isolated PRO polypeptide
CC scoring at least 80% positives when compared to any of the PRO
CC polypeptide sequences cited above (or an isolated PRO polypeptide having
CC at least 80% amino acid sequence identity to: (a) an amino acid sequence
CC encoded by the nucleotide deposited with ATCC numbers listed in the
CC specification; (b) the PRO polypeptide, lacking its associated signal
CC peptide; or (c) an extracellular domain of the PRO polypeptide, with or
CC lacking its associated signal peptide), a vector comprising the nucleic
CC acid molecule, a host cell comprising the vector (and producing a PRO
CC polypeptide), a chimaeric molecule comprising the PRO polypeptide fused
CC to a heterologous amino acid sequence and an anti-PRO antibody. The PRO
CC polypeptides or polynucleotides are useful as pharmaceuticals,
CC diagnostics, biosensors or bioreactors. These are particularly useful for
CC detecting or treating e.g. malignancies or cancers (e.g. ovarian cancer,
CC colorectal cancer, sarcoma, leukaemia or lymphoma), inflammatory disease,
CC necrosis, atherosclerosis, infertility, premature aging, psoriasis,
CC inflammatory disease, renal disease, arthritis, immune-mediated alopecia,
CC stroke, encephalitis, hepatitis, or multiple sclerosis in mammals. The
CC PRO polypeptides are useful in drug screening, particularly as targets
CC for therapeutic intervention in these diseases, and in the diagnostic
CC determination of the presence of these diseases. The PRO polypeptides are
CC also useful as molecular weight markers, or for chromosome
CC identification. The PRO genes are useful as hybridisation probes, or for
CC screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may
CC also be used in gene therapy, particularly for replacing a defective
CC gene. The present sequence represents a PRO polypeptide
XX
SQ Sequence 111 AA;

Query Match 100.0%; Score 587; DB 6; Length 111;
Best Local Similarity 100.0%; Pred. No. 8.9e-60;

Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60
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Db          1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60

Qy         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
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RESULT 13
ADA24909
ID ADA24909 standard; protein; 111 AA.
XX
AC ADA24909;
XX
DT 20-NOV-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO273.
XX
KW Human; secreted and transmembrane protein; PRO; tissue typing;
KW chromosome identification; vaccine; cancer; retinal disorder;
KW sports-related joint disorder; osteoarthritis; rheumatoid arthritis;
KW wound healing; obesity; diabetes; hearing loss;
KW cardiac insufficiency disorder; kidney disorder; nervous system disorder;
KW haemoglobin associated disorder.
XX
OS Homo sapiens.
XX
PN US2003050241-A1.
XX
PD 13-MAR-2003.
XX
PF 16-OCT-2001; 2001US-00978564.
XX
PR 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-0077450P.
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PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
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PR 20-MAR-1998; 98US-0078886P.
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PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079294P.
PR 26-MAR-1998; 98US-0079656P.
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PR 30-MAR-1998; 98US-0079923P.
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PR 31-MAR-1998; 98US-0080107P.
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PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
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PR 09-APR-1998; 98US-0081229P.

PR 15-APR-1998; 98US-0081817P.
PR 15-APR-1998; 98US-0081819P.
PR 15-APR-1998; 98US-0081838P.
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PR 21-APR-1998; 98US-0082568P.
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PR 22-APR-1998; 98US-0082700P.
PR 22-APR-1998; 98US-0082704P.
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PR 28-APR-1998; 98US-0083322P.
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PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 07-MAY-1998; 98US-0084643P.
PR 13-MAY-1998; 98US-0085323P.
PR 13-MAY-1998; 98US-0085338P.
PR 13-MAY-1998; 98US-0085339P.
PR 15-MAY-1998; 98US-0085573P.
PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085689P.
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PR 15-MAY-1998; 98US-0085700P.
PR 15-MAY-1998; 98US-0085704P.
PR 18-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086392P.
PR 22-MAY-1998; 98US-0086414P.
PR 22-MAY-1998; 98US-0086430P.
PR 22-MAY-1998; 98US-0086486P.
PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087106P.
PR 28-MAY-1998; 98US-0087208P.
PR 26-JUN-1998; 98US-0090863P.
PR 26-JUN-1998; 98US-0091010P.
PR 01-JUL-1998; 98US-0091359P.
PR 30-JUL-1998; 98US-0094651P.
PR 11-SEP-1998; 98US-0100038P.
PR 07-OCT-1998; 98WO-US021141.
PR 20-NOV-1998; 98US-0109304P.
PR 20-NOV-1998; 98WO-US024855.
PR 22-DEC-1998; 98US-0113296P.
PR 23-DEC-1998; 98US-0113621P.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 12-MAR-1999; 99US-0123957P.
PR 29-MAR-1999; 99US-0126773P.
PR 21-APR-1999; 99US-0130232P.
PR 26-APR-1999; 99US-0131022P.
PR 28-APR-1999; 99US-0131445P.
PR 14-MAY-1999; 99US-0134287P.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 16-JUN-1999; 99US-0139557P.
PR 23-JUN-1999; 99US-0141037P.
PR 07-JUL-1999; 99US-0142680P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
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PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001WO-US009552.
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PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-0091858S.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR WPI; 2003-521814/49.
DR N-PSDB; ADA24908.
XX
PT New isolated PRO polypeptides for example extracellular, secreted and
PT membrane bound proteins, useful for modulating the biological activities
PT of cells and for treating, for example diabetes, cancer, rheumatoid
PT arthritis, and hearing loss.
XX
PS Claim 12; Fig 149; 461pp; English.
XX
CC The invention describes an isolated secreted and transmembrane (PRO)
CC polypeptide (I). PRO337 polypeptide is useful for detecting PRO4993
CC polypeptide in a sample, and vice versa. PRO725, PRO700 and PRO739 are
CC useful for detecting PRO1559 polypeptide in a sample, and PRO1559 is
CC useful for detecting PRO725, PRO700 and PRO739 in a sample. PRO4993 is
CC useful for linking a bioactive molecule to a cell expressing a PRO337
CC polypeptide, and PRO337 is useful for linking a bioactive molecule to a
CC cell expressing a PRO4993 polypeptide. PRO1559 is useful for linking a
CC bioactive molecule to a cell expressing a PRO735, PRO700 and PRO739

Query Match 100.0%; Score 587; DB 6; Length 111;
Best Local Similarity 100.0%; Pred. No. 8.9e-60;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60

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Db         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111


RESULT 14
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ID   ABO19696 standard; protein; 111 AA.
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AC   ABO19696;
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DT   08-SEP-2003  (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO273.
XX
KW   Human; secreted and transmembrane protein; PRO; cell death; neuropathy;
KW   peripheral neuropathy; diabetic peripheral neuropathy;
KW   AIDS-associated neuropathy; Charcot-Marie-Tooth disease;
KW   Refusum's disease; Abetalipoproteinaemia; Tangier disease;
KW   Krabbe's disease; Metachromatic leukodystrophy; Fabry's disease;
KW   Dejerine-Sottas syndrome; chromosome mapping; gene mapping; gene therapy.
XX
OS   Homo sapiens.
XX
PN   US2003050240-A1.
XX
PD   13-MAR-2003.
XX
PF   16-OCT-2001; 2001US-00978403.
XX
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PR   01-JUL-1998;   98US-0091359P.
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PR   11-SEP-1998;   98US-0100038P.
PR   07-OCT-1998;   98WO-US021141.
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PR   20-NOV-1998;   98WO-US024855.
PR   22-DEC-1998;   98US-0113296P.
PR   23-DEC-1998;   98US-0113621P.
PR   05-JAN-1999;   99WO-US000106.
PR   08-MAR-1999;   99WO-US005028.
PR   10-MAR-1999;   99WO-US005190.
PR   12-MAR-1999;   99US-0123957P.
PR   29-MAR-1999;   99US-0126773P.
PR   21-APR-1999;   99US-0130232P.
PR   26-APR-1999;   99US-0131022P.
PR   28-APR-1999;   99US-0131445P.
PR   14-MAY-1999;   99US-0134287P.
PR   14-MAY-1999;   99WO-US010733.
PR   02-JUN-1999;   99WO-US012252.
PR   16-JUN-1999;   99US-0139557P.
PR   23-JUN-1999;   99US-0141037P.
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PR 07-JUL-1999; 99US-0142680P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001WO-US009552.
PR 25-MAY-2001; 2001WO-US017092.
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PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
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PA (GETH) GENENTECH INC.
XX
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PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WL;
XX
DR WPI; 2003-503575/47.
DR N-PSDB; ACD29919.
XX
PT Novel secreted and transmembrane polypeptide for modulating biological
PT activity of cell expressing the polypeptide, identifying agonists or
PT antagonists of polypeptide, and as molecular weight markers.
XX
PS Claim 12; Fig 149; 459pp; English.
XX
CC The invention describes an isolated, secreted and transmembrane
CC polypeptide, termed PRO polypeptide (I). (I) is useful for detecting
CC PRO4993, PRO337, PRO1559, PRO725, PRO700 or PRO739 polypeptide, and for
CC linking a bioactive molecule to a cell expressing the above polypeptides.
CC The bioactive molecule is a toxin, radiolabel or an antibody and causes
CC cell death. (I) is useful as therapeutic agent, in medical and industrial
CC applications e.g. for treating neuropathy, especially peripheral
CC neuropathy, diabetic peripheral neuropathy, AIDS-associated neuropathy,
CC Charcot-Marie-Tooth disease, Refusum's disease, Abetalipoproteinaemia,
CC Tangier disease, Krabbe's disease, Metachromatic leukodystrophy, Fabry's

Query Match 100.0%; Score 587; DB 6; Length 111;
Best Local Similarity 100.0%; Pred. No. 8.9e-60;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60
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Qy 61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
Db 61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111

RESULT 15
ADA12570
ID ADA12570 standard; protein; 111 AA.
XX
AC ADA12570;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human secreted/transmembrane polypeptide PRO273.
XX
KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;
KW infertility; birth defect; premature aging; AIDS; cancer;
KW diabetic complication; tissue typing; human.
XX
OS Homo sapiens.
XX
PN US2003055216-A1.
XX
PD 20-MAR-2003.
XX
PF 17-OCT-2001; 2001US-00978824.
XX
PR 21-MAY-1996; 96US-0018049P.
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PR 21-NOV-1997; 97US-0066364P.
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PR 26-MAR-1998; 98US-0079656P.
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PR 02-JUN-1999; 99WO-US012252.
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PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000US-00709238.
PR 27-NOV-2000; 2000US-00723749.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 22-MAR-2001; 2001US-00816920.
PR 22-MAR-2001; 2001WO-US009552.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 21-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;

Query Match 100.0%; Score 587; DB 6; Length 111;
Best Local Similarity 100.0%; Pred. No. 8.9e-60;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60

Qy         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
```

Search completed: April 22, 2004, 12:32:25
Job time : 58 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 22, 2004, 12:29:47 ; Search time 40 Seconds
(without alignments)
875.563 Million cell updates/sec

Title: US-09-978-189-370
Perfect score: 587
Sequence: 1 MSLLPRRAPPVSMRLLAAAL.....TKRPIKWYNAWNEKRRVYEE 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	582	99.1	111	4	Q9NS21	Q9ns21 homo sapien
2	507	86.4	99	11	Q8K453	Q8k453 rattus norv
3	506	86.2	99	11	Q9JHH7	Q9jhh7 mus musculu
4	488	83.1	95	11	Q91V02	Q91v02 mus musculu
5	335	57.1	100	13	Q9DFG4	Q9dfg4 brachydanio
6	322.5	54.9	98	13	Q9DGL8	Q9dgl8 gallus gall
7	143.5	24.4	101	11	Q9EP62	Q9ep62 rattus norv
8	128.5	21.9	108	6	Q28724	Q28724 oryctolagus
9	128	21.8	100	11	Q91ZK9	Q91zk9 sigmodon hi
10	126.5	21.6	101	11	Q91Z64	Q91z64 sigmodon hi
11	121.5	20.7	107	6	Q8HXZ4	Q8hxz4 macaca mula
12	119.5	20.4	107	6	Q8HXZ3	Q8hxz3 macaca mula
13	100	17.0	95	13	Q7T0B3	Q7t0b3 ictalurus p
14	97.5	16.6	97	13	Q98TQ2	Q98tq2 oncorhynchu
15	94.5	16.1	97	13	Q7SX73	Q7sx73 oncorhynchu
16	94.5	16.1	113	6	Q8MIN2	Q8min2 equus cabal
17	93.5	15.9	126	11	Q99J60	Q99j60 mus musculu
18	89.5	15.2	97	13	Q8QFP5	Q8qfp5 cyprinus ca
19	89.5	15.2	100	13	Q8AXP4	Q8axp4 chimaera ph
20	89.5	15.2	126	11	Q8C9J0	Q8c9j0 mus musculu
21	89	15.2	95	13	Q7T0B4	Q7t0b4 ictalurus p
22	89	15.2	113	11	Q9EQI5	Q9eqi5 mus musculu
23	88	15.0	95	13	Q7T0B2	Q7t0b2 ictalurus f
24	88	15.0	109	13	Q90Y59	Q90y59 paralichthy
25	87.5	14.9	111	11	Q99ME0	Q99me0 rattus norv
26	87	14.8	98	13	Q8QGV8	Q8qgv8 paralichthy
27	86.5	14.7	104	13	O73912	O73912 gallus gall
28	86	14.7	93	13	Q9PTF8	Q9ptf8 brachydanio
29	84.5	14.4	116	11	Q91ZB2	Q91zb2 mus musculu
30	84.5	14.4	117	11	Q8C9B8	Q8c9b8 mus musculu
31	83.5	14.2	102	6	Q95MZ7	Q95mz7 ovis aries
32	83.5	14.2	102	6	Q867B3	Q867b3 capra hircu
33	83.5	14.2	117	12	Q68398	Q68398 human cytom
34	83	14.1	94	6	Q8MIZ0	Q8miz0 macaca mula
35	81.5	13.9	101	13	Q8UW91	Q8uw91 triakis scy
36	80.5	13.7	98	6	Q8MIZ1	Q8miz1 macaca mula
37	80.5	13.7	98	6	Q865F5	Q865f5 macaca neme
38	79.5	13.5	101	6	Q7YRB5	Q7yrb5 tursiops tr
39	77.5	13.2	100	13	Q8QGB7	Q8qgb7 oncorhynchu
40	77.5	13.2	125	11	Q8K4B1	Q8k4b1 rattus norv
41	77	13.1	111	13	Q8AXZ1	Q8axz1 ictalurus p
42	76.5	13.0	59	6	O62764	O62764 equus cabal
43	76	12.9	98	11	Q9ERB1	Q9erb1 mesocricetu
44	76	12.9	98	13	Q7T1P1	Q7t1p1 cyprinus ca
45	76	12.9	677	5	O18209	O18209 caenorhabdi

ALIGNMENTS

RESULT 1
Q9NS21
ID Q9NS21 PRELIMINARY; PRT; 111 AA.
AC Q9NS21;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Chemokine MIP-2 gamma.
GN MIP-2 GAMMA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20405642; PubMed=10946286;
RA Cao X., Zhang W., Wan T., He L., Chen T., Yuan Z., Ma S., Yu Y.,
RA Chen G.;
RT "Molecular cloning and characterization of a novel CXC chemokine
RT macrophage inflammatory protein-2gamma chemoattractant for human
RT neutrophils and dendritic cells.";
RL J. Immunol. 165:2588-2595(2000).
DR EMBL; AF106911; AAF78449.1; -.
DR PIR; JG0182; JG0182.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
SQ SEQUENCE 111 AA; 13126 MW; C9A18B3178CACF74 CRC64;

Query Match 99.1%; Score 582; DB 4; Length 111;
Best Local Similarity 99.1%; Pred. No. 1e-58;
Matches 110; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 MSLLPRRAPPVSMRLLAAALLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSLLPRRAPPVSMRLLAAALLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60
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Qy          61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
               ||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db          61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRFYEE 111


RESULT 2
Q8K453
ID   Q8K453      PRELIMINARY;      PRT;    99 AA.
AC   Q8K453;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   BRAK.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Wistar;
RA   Han G.D., Koike H., Shimizu F., Kawachi H.;
RT   "Rat homolog of breast and kidney.";
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF488348; AAM74057.1; -.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0008009; F:chemokine activity; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   Pfam; PF00048; IL8; 1.
SQ   SEQUENCE   99 AA;  11730 MW;  972C06336C7F46D6 CRC64;

  Query Match             86.4%;  Score 507;  DB 11;  Length 99;
  Best Local Similarity   96.0%;  Pred. No. 3.4e-50;
  Matches   95;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          13 MRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIITT 72
               ||||||||||||||  :||||||||||||||||||||||||||||||||||||||||||
Db           1 MRLLAAALLLLLLALCASRVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIITT 60

Qy          73 KSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
               ||:|||||||||||||||||||||||||||||||||||
Db          61 KSMSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 99


RESULT 3
Q9JHH7
ID   Q9JHH7      PRELIMINARY;      PRT;    99 AA.
AC   Q9JHH7;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   B cell and mononcyte-activating chemokine precursor (Brain cDNA, clone
DE   MNCb-6413, similar to Mus musculus kidney-expressed chemokine CXC
DE   (Kec) mRNA) (Kec) (1200006I23Rik protein) (Small inducible cytokine
DE   subfamily B).
GN   CXCL14 OR SCYB14 OR BMAC OR 1200006I23RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/CBYJ;
RA   Sleeman M.A., Fraser J.K., Murison J.G., Kelly S.L., Prestidge R.,
RA   Watson J.D., Kumble K.D.;
RT   "B cell and monocyte-activating chemokine (BMAC), a novel non-ELR
RT   alpha chemokine.";
RL   Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL;
RA   Osada N., Kusuda J., Tanuma R., Ito A., Hirata M., Sugano S.,
RA   Hashimoto K.;
RT   "isolation of full-length cDNA clones from mouse brain cDNA library
RT   made by oligo-capping method.";
RL   Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Embryo, and Lung;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Body;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AF144754; AAF66694.1; -.
DR   EMBL; AB041614; BAA95097.1; -.
DR   EMBL; AK014351; BAB29292.1; -.
DR   EMBL; AK004615; BAB23411.1; -.
DR   EMBL; AK076112; BAC36192.1; -.
DR   MGD; MGI:1888514; Cxcl14.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0008009; F:chemokine activity; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   Pfam; PF00048; IL8; 1.
KW   Signal.
FT   SIGNAL        1     23       POTENTIAL.
FT   CHAIN        24     99       B CELL AND MONONCYTE-ACTIVATING
FT                                CHEMOKINE.
SQ   SEQUENCE   99 AA;  11716 MW;  97352E91FF7F46D6 CRC64;

  Query Match             86.2%;  Score 506;  DB 11;  Length 99;
  Best Local Similarity   94.9%;  Pred. No. 4.4e-50;
  Matches   94;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          13 MRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIITT 72
               ||||||||||||||  :||||||||||||||||||||||||||||||||||||||||:||
Db           1 MRLLAAALLLLLLALCASRVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIVTT 60

Qy          73 KSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
               ||:|||||||||||||||||||||||||||||||||||
Db          61 KSMSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 99


RESULT 4
Q91V02
ID   Q91V02      PRELIMINARY;      PRT;    95 AA.
AC   Q91V02;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
```

```
DE   MIP2gamma (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Placenta;
RA   Schilderink N., Geerts D.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF352784; AAK52902.1; -.
DR   EMBL; AF352785; AAK52903.1; -.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0008009; F:chemokine activity; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   Pfam; PF00048; IL8; 1.
FT   NON_TER       1       1
SQ   SEQUENCE   95 AA;  11202 MW;  EA9D0F5A7CA64F1C CRC64;

  Query Match             83.1%;  Score 488;  DB 11;  Length 95;
  Best Local Similarity   94.7%;  Pred. No. 4.8e-48;
  Matches   90;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         17 AAALLLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIITTKSVS 76
              |||||||||||  :||||||||||||||||||||||||||||||||||||||||:||||:|
Db          1 AAALLLLLLALCASRVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIVTTKSMS 60

Qy         77 RYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
              |||||||||||||||||||||||||||||||||||
Db         61 RYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 95


RESULT 5
Q9DFG4
ID   Q9DFG4      PRELIMINARY;      PRT;   100 AA.
AC   Q9DFG4;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   CXC-type chemokine.
GN   SCYBA.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20480374; PubMed=11025222;
RA   Long Q., Quint E., Lin S., Ekker M.;
RT   "The zebrafish scyba gene encodes a novel CXC-type chemokine with
RT   distinctive expression patterns in the vestibulo-acoustic system
RT   during embryogenesis.";
RL   Mech. Dev. 97:183-186(2000).
DR   EMBL; AF279919; AAG09819.1; -.
DR   ZFIN; ZDB-GENE-000619-1; scyba.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0008009; F:chemokine activity; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR001811; Chemokine_IL8.
SQ   SEQUENCE   100 AA;  12016 MW;  274BE255A74F98B5 CRC64;

  Query Match             57.1%;  Score 335;  DB 13;  Length 100;
  Best Local Similarity   54.6%;  Pred. No. 1.6e-30;
  Matches   53;  Conservative   25;  Mismatches   19;  Indels    0;  Gaps    0;

Qy         14 RLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIITTK 73
              |   ||| ||::|:|:   :  ||:|:||||||| ||:|||:||:|:|:|||: :| :
Db          3 RCSTAALFLLVIAVYSLNTEAYKCRCTRKGPKIRYIDVQKLEIKPKHPYCQEKMIFVTME 62

Qy         74 SVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYE 110
              :|||::|||:||||:||||:  :||:  | :| | :|
Db         63 NVSRFKGQEYCLHPRLQSTRNLVKWFKIWKDKHRTFE 99


RESULT 6
Q9DGL8
ID   Q9DGL8      PRELIMINARY;      PRT;    98 AA.
AC   Q9DGL8;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Jun-suppressed chemokine.
GN   JSC.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Fibroblast;
RA   Hartl M., Bister K.;
RT   "Suppression of genes in jun-transformed avian fibroblasts.";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF285876; AAG00529.1; -.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0008009; F:chemokine activity; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR001811; Chemokine_IL8.
SQ   SEQUENCE   98 AA;  11564 MW;  30D88E540AADD35B CRC64;

  Query Match             54.9%;  Score 322.5;  DB 13;  Length 98;
  Best Local Similarity   60.0%;  Pred. No. 4.1e-29;
  Matches   60;  Conservative   19;  Mismatches   18;  Indels    3;  Gaps    2;

Qy         13 MRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIITT 72
              |:|| |||||::|:  |  :| ||||||||||||:|:|:|||:||:|| | |:|:|:|
Db          1 MKLLTAALLLLVIAMCLASAEGVKCKCSRKGPKIRFSNVRKLEIKPRYPFCVEEMIIVTL 60

Qy         73 KSVSRYRG-QEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
                 :: || |:|||:|| |:| | :|||  | || |||||
Db         61 --WTKVRGEQQHCLNPKRQNTVRLLKWYRVWKEKGRVYEE 98


RESULT 7
Q9EP62
ID   Q9EP62      PRELIMINARY;      PRT;   101 AA.
AC   Q9EP62;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   CINC-2 alpha precursor.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Wistar; TISSUE=Peritoneal cavity;
RX   MEDLINE=98236997; PubMed=9576061;
RA   Shibata F., Konishi K., Nakagawa H.;
RT   "Gene structure, cDNA cloning, and expression of rat cytokine-induced
RT   neutrophil chemoattractant 2 (GRO/CINC-2) gene.";
RL   Cytokine 10:169-174(1998).
DR   EMBL; D87927; BAB12280.1; -.
DR   EMBL; D87926; BAB12279.1; -.
DR   HSSP; P10889; 1MI2.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0008009; F:chemokine activity; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   InterPro; IPR001089; CXC_chmkine_sm11.
DR   Pfam; PF00048; IL8; 1.
DR   PRINTS; PR00437; SMALLCYTKCXC.
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DR   SMART; SM00199; SCY; 1.
DR   PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
KW   Signal.
FT   SIGNAL        1     32       POTENTIAL.
FT   CHAIN        33    101       CINC-2 ALPHA.
SQ   SEQUENCE   101 AA;  11109 MW;  D949D5712FE30909 CRC64;

  Query Match             24.4%;  Score 143.5;  DB 11;  Length 101;
  Best Local Similarity   35.1%;  Pred. No. 1.3e-08;
  Matches   34;  Conservative   19;  Mismatches   31;  Indels   13;  Gaps    3;

Qy          8 APPVSMRLLAAALLLLLLALYTARVDGS-------KCKCSRKGPKIRYSDVKKLEMKPKY 60
              ||| : ||| |||||||| : |:            :|:| :  |:: : ::: | : |
Db          2 APP-TRRLLNAALLLLLLLMATSHQPSGTVVARELRCQCLKTLPRVDFENIQSLTVTPPG 60

Qy         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIK 97
              ||| :  || | |      ||| ||:|:    :: |:
Db         61 PHCTQTEVIATLKD-----GQEVCLNPQAPRLQKIIQ 92


RESULT 8
Q28724
ID   Q28724      PRELIMINARY;      PRT;   108 AA.
AC   Q28724;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-AUG-1999 (TrEMBLrel. 11, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   GRO (Permeability factor 2).
GN   RPF2.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NEW ZEALAND WHITE;
RA   Yoshimura T., Modi W.S.;
RT   "Isolation of novel GRO genes, and a phylogenetic analysis of the CXC
RT   chemokine subfamily in mammals.";
RL   Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 43-108 FROM N.A.
RC   STRAIN=NEW ZEALAND WHITE;
RX   MEDLINE=95129889; PubMed=7828903;
RA   Johnson M.C., Goodman R.B. II, Kajikawa O., Wong V.A., Mongovin S.M.,
RA   Martin T.R.;
RT   "Cloning of two rabbit GRO homologues and their expression in alveolar
RT   macrophages.";
RL   Gene 151:337-338(1994).
DR   EMBL; U95808; AAB93924.1; -.
DR   EMBL; L28933; AAA66975.1; -.
DR   PIR; S17507; S17507.
DR   HSSP; P19875; 1QNK.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0008009; F:chemokine activity; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   InterPro; IPR001089; CXC_chmkine_sml1.
DR   Pfam; PF00048; IL8; 1.
DR   PRINTS; PR00437; SMALLCYTKCXC.
DR   SMART; SM00199; SCY; 1.
DR   PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
SQ   SEQUENCE   108 AA;  11261 MW;  9C278041FC7A5BAD CRC64;

  Query Match             21.9%;  Score 128.5;  DB 6;  Length 108;
  Best Local Similarity   33.3%;  Pred. No. 7e-07;
  Matches   32;  Conservative   15;  Mismatches   38;  Indels   11;  Gaps    2;

Qy          8 APPVSMRLLAAALLLLLLALYTARVDGS------KCKCSRKGPKIRYSDVKKLEMKPKYP 61
              | |   | |  |:|||||   : |  |:      :|:| :    |    :: |::   |
Db          9 AAPSGPRFLRTAMLLLLLLAASRRAAGAAALTELRCQCLQTVQGIHLKSIQSLKVLSPGP 68

Qy         62 HCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIK 97
              || :  || | ||      ||| ||:|:    :|::
Db         69 HCAQTEVIATLKS-----GQEACLNPAAPMVKKFLQ 99


RESULT 9
Q91ZK9
ID   Q91ZK9      PRELIMINARY;      PRT;   100 AA.
AC   Q91ZK9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Growth-regulated protein.
GN   GRO.
OS   Sigmodon hispidus (Hispid cotton rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC   Sigmodon.
OX   NCBI_TaxID=42415;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Blanco J.C., Pletneva L.M., Prince G.A.;
RT   "Sigmodon hispidus cytokines, chemokines and interferons.";
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF421393; AAL16934.1; -.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0008009; F:chemokine activity; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   InterPro; IPR001089; CXC_chmkine_sml1.
DR   Pfam; PF00048; IL8; 1.
DR   PRINTS; PR00437; SMALLCYTKCXC.
DR   SMART; SM00199; SCY; 1.
DR   PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
SQ   SEQUENCE   100 AA;  10686 MW;  B357C8C6F002057C CRC64;

  Query Match             21.8%;  Score 128;  DB 11;  Length 100;
  Best Local Similarity   32.3%;  Pred. No. 7.3e-07;
  Matches   31;  Conservative   21;  Mismatches   32;  Indels   12;  Gaps    3;

Qy          8 APPVSMRLLAAALLLLLLALYTARVDGS------KCKCSRKGPKIRYSDVKKLEMKPKYP 61
              ||     | ||||||||||  : :  |:      :|:| :    : : ::: |:: | |
Db          2 APATRPLLRAAALLLLLLAA-SRQTTGAPVANELRCQCLQTMAGVHFKNIQSLKVTPPGP 60

Qy         62 HCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIK 97
              || :  || | |:      ||| ||:|:    :: ::
Db         61 HCTQTEVIATLKN-----GQEACLNPEAPMVQKIVQ 91


RESULT 10
Q91Z64
ID   Q91Z64      PRELIMINARY;      PRT;   101 AA.
AC   Q91Z64;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Macrophage inflammatory protein-2.
GN   MIP2.
OS   Sigmodon hispidus (Hispid cotton rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC   Sigmodon.
OX   NCBI_TaxID=42415;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Blanco J.C., Pletneva L.M., Prince G.A.;
RT   "Sigmodon hispidus cytokines, chemokines and interferons.";
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY059408; AAL26705.1; -.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0008009; F:chemokine activity; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   InterPro; IPR001089; CXC_chmkine_sml1.
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DR   Pfam; PF00048; IL8; 1.
DR   PRINTS; PR00437; SMALLCYTKCXC.
DR   SMART; SM00199; SCY; 1.
DR   PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
SQ   SEQUENCE   101 AA;  11018 MW;  FC1C5F36A8C2A443 CRC64;

  Query Match             21.6%;  Score 126.5;  DB 11;  Length 101;
  Best Local Similarity   31.2%;  Pred. No. 1.1e-06;
  Matches   30;  Conservative   21;  Mismatches   34;  Indels   11;  Gaps    2;

Qy          8 APPVSMRLLAAALLLLLLALYTARVDGS------KCKCSRKGPKIRYSDVKKLEMKPKYP 61
              ||  |: | :| ||||||     :  |:      :|:| :   :| :  :: |:: | |
Db          2 APTTSLFLRSAMLLLLLLVATHRQATGAVLATELRCQCVKTLQRIDFKTIQSLKVTPPGP 61

Qy         62 HCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIK 97
              || :  || | |:     ||: ||:|:    :: |:
Db         62 HCTQTEVIATLKN-----GQDVCLNPEAPLVQKIIQ 92


RESULT 11
Q8HXZ4
ID   Q8HXZ4      PRELIMINARY;      PRT;   107 AA.
AC   Q8HXZ4;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Chemokine CXCL1/GRO-alpha.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Basu S., Schaefer T.M., Ghosh M., Fuller C.L., Reinhart T.A.;
RT   "Comprehensive cloning and sequencing reveals evolutionary
RT   conservation among all groups of rhesus macaque chemokines.";
RL   Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF449280; AAN76084.1; -.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0008009; F:chemokine activity; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   InterPro; IPR001089; CXC_chmkine_sml1.
DR   Pfam; PF00048; IL8; 1.
DR   PRINTS; PR00437; SMALLCYTKCXC.
DR   SMART; SM00199; SCY; 1.
DR   PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
SQ   SEQUENCE   107 AA;  11355 MW;  CDDC2F86449923C4 CRC64;

  Query Match             20.7%;  Score 121.5;  DB 6;  Length 107;
  Best Local Similarity   33.3%;  Pred. No. 4.4e-06;
  Matches   32;  Conservative   15;  Mismatches   38;  Indels   11;  Gaps    2;

Qy          8 APPVSMRLLAAALLLLLLALYTARVDGS------KCKCSRKGPKIRYSDVKKLEMKPKYP 61
              | | : | |  |||||||      |  |:      :|:| :    |   ::: : :|   |
Db          8 AAPSNPRFLQVALLLLLLVATGRRAAGASVVTELRCQCLQTLQGIHPKNIQSVNVKAPGP 67

Qy         62 HCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIK 97
              || |  || | |:     ||: ||:|    :: ||
Db         68 HCAETEVIATLKN-----GQKACLNPASPMVQKIIK 98


RESULT 12
Q8HXZ3
ID   Q8HXZ3      PRELIMINARY;      PRT;   107 AA.
AC   Q8HXZ3;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Chemokine CXCL3/GRO-gamma.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Basu S., Schaefer T.M., Ghosh M., Fuller C.L., Reinhart T.A.;
RT   "Comprehensive cloning and sequencing reveals evolutionary
RT   conservation among all groups of rhesus macaque chemokines.";
RL   Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF449282; AAN76085.1; -.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0008009; F:chemokine activity; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   InterPro; IPR001089; CXC_chmkine_sml1.
DR   Pfam; PF00048; IL8; 1.
DR   PRINTS; PR00437; SMALLCYTKCXC.
DR   SMART; SM00199; SCY; 1.
DR   PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
SQ   SEQUENCE   107 AA;  11294 MW;  E5999B36BC523EBD CRC64;

  Query Match             20.4%;  Score 119.5;  DB 6;  Length 107;
  Best Local Similarity   33.3%;  Pred. No. 7.4e-06;
  Matches   32;  Conservative   16;  Mismatches   37;  Indels   11;  Gaps    2;

Qy          8 APPVSMRLLAAALLLLLLALYTARVDGS------KCKCSRKGPKIRYSDVKKLEMKPKYP 61
              | | : |||  |||||||      |  |:      :|:| :    |   ::: : :|   |
Db          8 AAPSNPRLLRVALLLLLLVATGRRATGAPVATELRCQCLQTLQGIHPKNIQSVIVKAPGP 67

Qy         62 HCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIK 97
              || |  || | |:     ||: ||:|    :: |:
Db         68 HCAETEVIATLKN-----GQKACLNPASPMVQKIIE 98


RESULT 13
Q7T0B3
ID   Q7T0B3      PRELIMINARY;      PRT;    95 AA.
AC   Q7T0B3;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Chemokine.
GN   CXCL10.
OS   Ictalurus punctatus (Channel catfish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC   Ictaluridae; Ictalurus.
OX   NCBI_TaxID=7998;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Baoprasertkul P., Peatman E., Kucuktas H., Li P., He C., Chen L.,
RA   Simmons M., Liu Z.;
RT   "Differential Expression Profiles of Chemokine CXCL10 in Resistant and
RT   Susceptible Catfish after Infection of Edwardsiella Ictaluri.";
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY335950; AAQ01586.1; -.
SQ   SEQUENCE   95 AA;  10340 MW;  EB5CF92D3070DD58 CRC64;

  Query Match             17.0%;  Score 100;  DB 13;  Length 95;
  Best Local Similarity   31.9%;  Pred. No. 0.0011;
  Matches   29;  Conservative   17;  Mismatches   33;  Indels   12;  Gaps    4;

Qy         19 ALLLLLLALYTARVDGSKCKCSRKGPK---IRYSDVKKLEMKPKYPHCEEKMVIITTKSV 75
              | ||::    ||    :| |  :||    :|   : |:|: |    || | :|:| |:
Db         11 ACLLIVHVQGQARTSVRRCLC--QGPAANGVRLQRIDKIEIHPASATCENKEIIVTLKN- 67

Qy         76 SRYRGQEHCLHPKLQSTKRFIKWYNAWNEKR 106
                 : ||:|: : ||::|    |  |||
Db         68 ---GAGKKCLNPESEFTKKYI---TAALEKR 92


RESULT 14
Q98TQ2
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ID   Q98TQ2      PRELIMINARY;      PRT;    97 AA.
AC   Q98TQ2;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Interleukin-8 (Putative cxc chemokine precursor).
GN   IL-8.
OS   Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX   NCBI_TaxID=8022;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Laing K.J., Zou J.J., Hirono I., Aoki T., Secombes C.J.;
RT   "Identification and analysis of the interleukin 8 molecule in rainbow
RT   trout Oncorhynchus mykiss.";
RL   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RA   Sangrador-Vegas A., Smith T.J.;
RT   "Molecular cloning of a rainbow trout (Oncorhynchus mykiss) CXC
RT   chemokine by use of suppression subtractive hybridization.";
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Laing K.J., Zou J.J., Hirono I., Aoki T., Secombes C.J.;
RT   "Identification and analysis of the interleukin 8 molecule in rainbow
RT   trout Oncorhynchus mykiss.";
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22642999; PubMed=12695860;
RA   Fujiki K., Gauley J., Bols N.C., Dixon B.;
RT   "Genomic cloning of novel isotypes of the rainbow trout interleukin-
RT   8.";
RL   Immunogenetics 55:126-131(2003).
DR   EMBL; AJ279069; CAC33585.1; -.
DR   EMBL; AJ300835; CAC45061.1; -.
DR   EMBL; AJ310565; CAC83945.1; -.
DR   EMBL; AY160982; AAO25641.1; -.
DR   EMBL; AY160983; AAO25642.1; -.
DR   EMBL; AY160984; AAO25643.1; -.
DR   EMBL; AY160985; AAO25644.1; -.
DR   EMBL; AY160986; AAO25645.1; -.
DR   HSSP; P19875; 1QNK.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0008009; F:chemokine activity; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   Pfam; PF00048; IL8; 1.
DR   SMART; SM00199; SCY; 1.
KW   Signal.
FT   SIGNAL        1     22       POTENTIAL.
FT   CHAIN        23     97       PUTATIVE CXC CHEMOKINE.
SQ   SEQUENCE   97 AA;  10777 MW;  4EEB35A4EF9DACE2 CRC64;

  Query Match             16.6%;  Score 97.5;  DB 13;  Length 97;
  Best Local Similarity   34.0%;  Pred. No. 0.0022;
  Matches   34;  Conservative   18;  Mismatches   25;  Indels   23;  Gaps    6;

Qy          11 VSMRLLAAALLLLLLALYTARVDGS--------KCKC----SRKGPKIRYSDVKKLEMKP 58
               :|:| ::|:|:::|||| |      |        :|:|    ||:  |:    :||:|| |
Db           1 MSIR-MSASLVVVLLALLTITEGMSLRGMGADLRCRCIETESRRIGKL----IKKVEMFP 55

Qy          59 KYPHCEEKMVIIT-TKSVSRYRGQEHCLHPKLQSTKRFIK 97
                 || :  :| | :||     ||| ||       || |:
Db          56 PSSHCRDTEIIATLSKS-----GQEICLDVSAPWVKRVIE 90


RESULT 15
Q7SX73
```

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ID   Q7SX73      PRELIMINARY;      PRT;    97 AA.
AC   Q7SX73;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Interleukin-8 (Interleukin 8X).
GN   IL-8.
OS   Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX   NCBI_TaxID=8022;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22642999; PubMed=12695860;
RA   Fujiki K., Gauley J., Bols N.C., Dixon B.;
RT   "Genomic cloning of novel isotypes of the rainbow trout interleukin-
RT   8.";
RL   Immunogenetics 55:126-131(2003).
DR   EMBL; AY160981; AAO25640.1; -.
DR   EMBL; AY160987; AAO25646.1; -.
DR   EMBL; AY221022; AAP42829.1; -.
SQ   SEQUENCE   97 AA;  10749 MW;  4EEB2A99EF9DACE2 CRC64;

  Query Match             16.1%;  Score 94.5;  DB 13;  Length 97;
  Best Local Similarity   33.0%;  Pred. No. 0.0048;
  Matches   33;  Conservative   19;  Mismatches   25;  Indels   23;  Gaps    6;

Qy          11 VSMRLLAAALLLLLLALYTARVDGS--------KCKC----SRKGPKIRYSDVKKLEMKP 58
               :|:| ::|:|:::|||| |      |        :|:|    ||:  |:    :||:|| |
Db           1 MSIR-MSASLVVVLLALLTITEGMSLRGMGADLRCRCIETESRRIGKL----IKKVEMFP 55

Qy          59 KYPHCEEKMVIIT-TKSVSRYRGQEHCLHPKLQSTKRFIK 97
                 || :  :| | :||     ||| ||       |: |:
Db          56 PSSHCRDTEIIATLSKS-----GQEICLDVSAPWVKKVIE 90


Search completed: April 22, 2004, 12:33:47
Job time : 42 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 22, 2004, 12:31:18 ; Search time 22 Seconds
(without alignments)
260.476 Million cell updates/sec

Title: US-09-978-189-370
Perfect score: 587
Sequence: 1 MSLLPRRAPPVSMRLLAAAL.....TKRFIKWYNAWNEKRRVYEE 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	582	99.1	111	2	US-08-825-556A-2	Sequence 2, Appli
2	582	99.1	111	4	US-09-238-184-2	Sequence 2, Appli
3	522	88.9	99	2	US-08-825-556A-3	Sequence 3, Appli
4	522	88.9	99	4	US-09-238-184-3	Sequence 3, Appli
5	509	86.7	95	3	US-09-188-930-344	Sequence 344, App
6	509	86.7	95	4	US-09-724-864-68	Sequence 68, Appl
7	509	86.7	95	4	US-09-312-283C-344	Sequence 344, App
8	506	86.2	99	3	US-09-188-930-340	Sequence 340, App
9	506	86.2	99	4	US-09-312-283C-340	Sequence 340, App
10	506	86.2	99	4	US-09-312-283C-394	Sequence 394, App
11	506	86.2	99	4	US-09-312-283C-417	Sequence 417, App
12	504.5	85.9	98	4	US-09-312-283C-418	Sequence 418, App
13	428	72.9	77	3	US-09-188-930-346	Sequence 346, App
14	428	72.9	77	4	US-09-724-864-72	Sequence 72, Appl
15	428	72.9	77	4	US-09-312-283C-346	Sequence 346, App
16	424	72.2	77	3	US-09-188-930-345	Sequence 345, App
17	424	72.2	77	4	US-09-724-864-70	Sequence 70, Appl
18	424	72.2	77	4	US-09-312-283C-345	Sequence 345, App
19	414	70.5	75	4	US-09-177-304-3	Sequence 3, Appli
20	298	50.8	133	3	US-09-188-930-157	Sequence 157, App
21	298	50.8	133	4	US-09-312-283C-157	Sequence 157, App
22	143.5	24.4	98	2	US-08-825-556A-4	Sequence 4, Appli
23	143.5	24.4	98	4	US-09-238-184-4	Sequence 4, Appli
24	143.5	24.4	100	4	US-08-679-493A-146	Sequence 146, App
25	138	23.5	100	3	US-08-476-376-2	Sequence 2, Appli
26	138	23.5	100	4	US-09-312-283C-423	Sequence 423, App
27	128.5	21.9	107	1	US-08-352-324A-4	Sequence 4, Appli
28	128.5	21.9	107	2	US-08-862-607-4	Sequence 4, Appli
29	128.5	21.9	107	2	US-08-468-819-6	Sequence 6, Appli
30	128.5	21.9	107	3	US-09-203-235-4	Sequence 4, Appli
31	128.5	21.9	107	4	US-09-213-383-6	Sequence 6, Appli
32	128.5	21.9	107	5	PCT-US95-16144-4	Sequence 4, Appli
33	117.5	20.0	107	1	US-08-352-324A-7	Sequence 7, Appli
34	117.5	20.0	107	2	US-08-862-607-7	Sequence 7, Appli
35	117.5	20.0	107	2	US-08-468-819-5	Sequence 5, Appli
36	117.5	20.0	107	3	US-09-203-235-7	Sequence 7, Appli
37	117.5	20.0	107	4	US-09-213-383-5	Sequence 5, Appli
38	117.5	20.0	107	5	PCT-US95-16144-7	Sequence 7, Appli
39	113	19.3	71	2	US-08-812-003-9	Sequence 9, Appli
40	111	18.9	96	4	US-08-649-006A-7	Sequence 7, Appli
41	111	18.9	96	4	US-09-771-023-9	Sequence 9, Appli
42	111	18.9	96	4	US-09-312-283C-424	Sequence 424, App
43	109	18.6	106	4	US-08-679-493A-148	Sequence 148, App
44	107	18.2	106	1	US-08-352-324A-5	Sequence 5, Appli
45	107	18.2	106	2	US-08-862-607-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-08-825-556A-2
; Sequence 2, Application US/08825556A
; Patent No. 5910431
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Su, Jeffrey Y.
; APPLICANT: Li, Haodong
; TITLE OF INVENTION: Chemokine Alpha 2
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-2934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/825,556A
; FILING DATE: 19-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,653
; FILING DATE: 19-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0850001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-825-556A-2

Query Match 99.1%; Score 582; DB 2; Length 111;
Best Local Similarity 99.1%; Pred. No. 1.4e-63;
Matches 110; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60

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Db          1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60

Qy         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
               ||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRFYEE 111


RESULT 2
US-09-238-184-2
; Sequence 2, Application US/09238184
; Patent No. 6479633
;  GENERAL INFORMATION:
;    APPLICANT:  Ni, Jian
;    APPLICANT:  Gentz, Reiner L.
;    APPLICANT:  Su, Jeffrey Y.
;    APPLICANT:  Li, Haodong
;    TITLE OF INVENTION:  Chemokine Alpha 2
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox, P.L.L.C.
;      STREET:  1100 New York Ave., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-2934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/238,184
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/825,556
;      FILING DATE:  19-MAR-1997
;      APPLICATION NUMBER:  US 60/013,653
;      FILING DATE:  19-MAR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steffe, Eric K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.0850001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  111 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-238-184-2

  Query Match             99.1%;  Score 582;  DB 4;  Length 111;
  Best Local Similarity   99.1%;  Pred. No. 1.4e-63;
  Matches  110;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKY 60

Qy         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
               ||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db         61 PHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRFYEE 111


RESULT 3
US-08-825-556A-3
; Sequence 3, Application US/08825556A
; Patent No. 5910431
;  GENERAL INFORMATION:
;    APPLICANT:  Ni, Jian
;    APPLICANT:  Gentz, Reiner L.
;    APPLICANT:  Su, Jeffrey Y.
;    APPLICANT:  Li, Haodong
;    TITLE OF INVENTION:  Chemokine Alpha 2
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox, P.L.L.C.
;      STREET:  1100 New York Ave., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-2934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/825,556A
;      FILING DATE:  19-MAR-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/013,653
;      FILING DATE:  19-MAR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steffe, Eric K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.0850001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  99 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-825-556A-3

  Query Match             88.9%;  Score 522;  DB 2;  Length 99;
  Best Local Similarity   99.0%;  Pred. No. 2.6e-56;
  Matches   98;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         13 MRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIITT 72
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIITT 60

Qy         73 KSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
              |||||||||||||||||||||||||||||||||||| |||
Db         61 KSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRFYEE 99


RESULT 4
US-09-238-184-3
; Sequence 3, Application US/09238184
; Patent No. 6479633
;  GENERAL INFORMATION:
;    APPLICANT:  Ni, Jian
;    APPLICANT:  Gentz, Reiner L.
;    APPLICANT:  Su, Jeffrey Y.
;    APPLICANT:  Li, Haodong
;    TITLE OF INVENTION:  Chemokine Alpha 2
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox, P.L.L.C.
;      STREET:  1100 New York Ave., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-2934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
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;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/238,184
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/825,556
;       FILING DATE:  19-MAR-1997
;       APPLICATION NUMBER:  US 60/013,653
;       FILING DATE:  19-MAR-1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Steffe, Eric K.
;       REGISTRATION NUMBER:  36,688
;       REFERENCE/DOCKET NUMBER:  1488.0850001
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-371-2600
;       TELEFAX:  202-371-2540
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  99 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-09-238-184-3

  Query Match             88.9%;  Score 522;  DB 4;  Length 99;
  Best Local Similarity   99.0%;  Pred. No. 2.6e-56;
  Matches   98;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          13 MRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIITT 72
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 MRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIITT 60

Qy          73 KSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
               |||||||||||||||||||||||||||||||||||| |||
Db          61 KSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRFYEE 99


RESULT 5
US-09-188-930-344
; Sequence 344, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
;  APPLICANT: Watson, James D.
;  APPLICANT: Strachan, Lorna
;  APPLICANT: Sleeman, Matthew
;  APPLICANT: Onrust, Rene
;  APPLICANT: Murison, James Greg
;  TITLE OF INVENTION: Compositions Isolated From Skin Cells
;  TITLE OF INVENTION: and Methods For Their Use
;  FILE REFERENCE: 11000.1011c1
;  CURRENT APPLICATION NUMBER: US/09/188,930A
;  CURRENT FILING DATE: 1998-11-09
;  NUMBER OF SEQ ID NOS: 348
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 344
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Mouse
US-09-188-930-344

  Query Match             86.7%;  Score 509;  DB 3;  Length 95;
  Best Local Similarity   100.0%;  Pred. No. 9.5e-55;
  Matches   95;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          17 AAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIITTKSVS 76
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 AAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIITTKSVS 60

Qy          77 RYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
               |||||||||||||||||||||||||||||||||||
Db          61 RYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 95


RESULT 6
US-09-724-864-68
; Sequence 68, Application US/09724864
; Patent No. 6380362
; GENERAL INFORMATION:
;  APPLICANT:  Watson, James D
;  APPLICANT:  Murison, James G.
;  TITLE OF INVENTION:  Polynucleotides, polypeptides expressed
;  TITLE OF INVENTION:  by the polynucleotides and methods for their use.
;  FILE REFERENCE:  11000.1050U1
;  CURRENT APPLICATION NUMBER: US/09/724,864
;  CURRENT FILING DATE:  2000-11-28
;  PRIOR APPLICATION NUMBER:  U.S. No. 6380362 60/171,678
;  PRIOR FILING DATE:  1999-12-23
;  NUMBER OF SEQ ID NOS:  72
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 68
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Human
US-09-724-864-68

  Query Match             86.7%;  Score 509;  DB 4;  Length 95;
  Best Local Similarity   100.0%;  Pred. No. 9.5e-55;
  Matches   95;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          17 AAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIITTKSVS 76
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 AAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIITTKSVS 60

Qy          77 RYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
               |||||||||||||||||||||||||||||||||||
Db          61 RYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 95


RESULT 7
US-09-312-283C-344
; Sequence 344, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
;  APPLICANT: Watson, James D.
;  APPLICANT:  Strachan, Lorna
;  APPLICANT:  Sleeman, Matthew
;  APPLICANT:  Onrust, Rene
;  APPLICANT:  Murison, James G.
;  APPLICANT:  Kumble, Krishanand D.
;  TITLE OF INVENTION: Compositions Isolated from Skin Cells
;  TITLE OF INVENTION:  and Methods for Their Use
;  FILE REFERENCE: 11000.1011c2
;  CURRENT APPLICATION NUMBER: US/09/312,283C
;  CURRENT FILING DATE:  1999-05-14
;  NUMBER OF SEQ ID NOS: 425
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 344
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Mouse
US-09-312-283C-344

  Query Match             86.7%;  Score 509;  DB 4;  Length 95;
  Best Local Similarity   100.0%;  Pred. No. 9.5e-55;
  Matches   95;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          17 AAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIITTKSVS 76
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 AAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIITTKSVS 60

Qy          77 RYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
               |||||||||||||||||||||||||||||||||||
Db          61 RYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 95
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RESULT 8
US-09-188-930-340
; Sequence 340, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 340
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Mouse
US-09-188-930-340

Query Match 86.2%; Score 506; DB 3; Length 99;
Best Local Similarity 94.9%; Pred. No. 2.3e-54;
Matches 94; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 13 MRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIITT 72
Db 1 MRLLAAALLLLLLALCASRVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIVTT 60

Qy 73 KSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
Db 61 KSMSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 99

RESULT 9
US-09-312-283C-340
; Sequence 340, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011c2
; CURRENT APPLICATION NUMBER: US/09/312,283C
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 340
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Mouse
US-09-312-283C-340

Query Match 86.2%; Score 506; DB 4; Length 99;
Best Local Similarity 94.9%; Pred. No. 2.3e-54;
Matches 94; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 13 MRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIITT 72
Db 1 MRLLAAALLLLLLALCASRVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIVTT 60

Qy 73 KSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
Db 61 KSMSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 99

RESULT 10
US-09-312-283C-394
; Sequence 394, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011c2
; CURRENT APPLICATION NUMBER: US/09/312,283C
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 394
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Mouse
US-09-312-283C-394

Query Match 86.2%; Score 506; DB 4; Length 99;
Best Local Similarity 94.9%; Pred. No. 2.3e-54;
Matches 94; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 13 MRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIITT 72
Db 1 MRLLAAALLLLLLALCASRVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIVTT 60

Qy 73 KSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
Db 61 KSMSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 99

RESULT 11
US-09-312-283C-417
; Sequence 417, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011c2
; CURRENT APPLICATION NUMBER: US/09/312,283C
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 417
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Mouse
US-09-312-283C-417

Query Match 86.2%; Score 506; DB 4; Length 99;
Best Local Similarity 94.9%; Pred. No. 2.3e-54;
Matches 94; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 13 MRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIITT 72
Db 1 MRLLAAALLLLLLALCASRVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIVTT 60

Qy 73 KSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111

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Db         61 KSMSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 99


RESULT 12
US-09-312-283C-418
; Sequence 418, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
;  APPLICANT: Watson, James D.
;  APPLICANT:  Strachan, Lorna
;  APPLICANT:  Sleeman, Matthew
;  APPLICANT:  Onrust, Rene
;  APPLICANT:  Murison, James G.
;  APPLICANT:  Kumble, Krishanand D.
;  TITLE OF INVENTION: Compositions Isolated from Skin Cells
;  TITLE OF INVENTION:  and Methods for Their Use
;  FILE REFERENCE: 11000.1011c2
;  CURRENT APPLICATION NUMBER: US/09/312,283C
;  CURRENT FILING DATE:  1999-05-14
;  NUMBER OF SEQ ID NOS: 425
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 418
;   LENGTH: 98
;   TYPE: PRT
;   ORGANISM: Human
US-09-312-283C-418

  Query Match            85.9%;  Score 504.5;  DB 4;  Length 98;
  Best Local Similarity   98.0%;  Pred. No. 3.5e-54;
  Matches   97;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy         13 MRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIITT 72
              ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db          1 MRLPAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVII-T 59

Qy         73 KSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 111
              |||||||||||||||||||||||||||||||||||||||
Db         60 KSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNEKRRVYEE 98


RESULT 13
US-09-188-930-346
; Sequence 346, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
;  APPLICANT: Watson, James D.
;  APPLICANT: Strachan, Lorna
;  APPLICANT: Sleeman, Matthew
;  APPLICANT: Onrust, Rene
;  APPLICANT: Murison, James Greg
;  TITLE OF INVENTION: Compositions Isolated From Skin Cells
;  TITLE OF INVENTION: and Methods For Their Use
;  FILE REFERENCE: 11000.1011c1
;  CURRENT APPLICATION NUMBER: US/09/188,930A
;  CURRENT FILING DATE: 1998-11-09
;  NUMBER OF SEQ ID NOS: 348
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 346
;   LENGTH: 77
;   TYPE: PRT
;   ORGANISM: Mouse
US-09-188-930-346

  Query Match            72.9%;  Score 428;  DB 3;  Length 77;
  Best Local Similarity   100.0%;  Pred. No. 5.9e-45;
  Matches   77;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         35 SKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKR 94
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 SKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKR 60

Qy         95 FIKWYNAWNEKRRVYEE 111
              |||||||||||||||||
Db         61 FIKWYNAWNEKRRVYEE 77


RESULT 14
US-09-724-864-72
; Sequence 72, Application US/09724864
; Patent No. 6380362
; GENERAL INFORMATION:
;  APPLICANT:  Watson, James D
;  APPLICANT:  Murison, James G.
;  TITLE OF INVENTION:  Polynucleotides, polypeptides expressed
;  TITLE OF INVENTION:  by the polynucleotides and methods for their use.
;  FILE REFERENCE:  11000.1050U1
;  CURRENT APPLICATION NUMBER: US/09/724,864
;  CURRENT FILING DATE:  2000-11-28
;  PRIOR APPLICATION NUMBER:  U.S. No. 6380362 60/171,678
;  PRIOR FILING DATE:  1999-12-23
;  NUMBER OF SEQ ID NOS:  72
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 72
;   LENGTH: 77
;   TYPE: PRT
;   ORGANISM: Human
US-09-724-864-72

  Query Match            72.9%;  Score 428;  DB 4;  Length 77;
  Best Local Similarity   100.0%;  Pred. No. 5.9e-45;
  Matches   77;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         35 SKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKR 94
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 SKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKR 60

Qy         95 FIKWYNAWNEKRRVYEE 111
              |||||||||||||||||
Db         61 FIKWYNAWNEKRRVYEE 77


RESULT 15
US-09-312-283C-346
; Sequence 346, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
;  APPLICANT: Watson, James D.
;  APPLICANT:  Strachan, Lorna
;  APPLICANT:  Sleeman, Matthew
;  APPLICANT:  Onrust, Rene
;  APPLICANT:  Murison, James G.
;  APPLICANT:  Kumble, Krishanand D.
;  TITLE OF INVENTION: Compositions Isolated from Skin Cells
;  TITLE OF INVENTION:  and Methods for Their Use
;  FILE REFERENCE: 11000.1011c2
;  CURRENT APPLICATION NUMBER: US/09/312,283C
;  CURRENT FILING DATE:  1999-05-14
;  NUMBER OF SEQ ID NOS: 425
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 346
;   LENGTH: 77
;   TYPE: PRT
;   ORGANISM: Mouse
US-09-312-283C-346

  Query Match            72.9%;  Score 428;  DB 4;  Length 77;
  Best Local Similarity   100.0%;  Pred. No. 5.9e-45;
  Matches   77;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         35 SKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKR 94
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 SKCKCSRKGPKIRYSDVKKLEMKPKYPHCEEKMVIITTKSVSRYRGQEHCLHPKLQSTKR 60

Qy         95 FIKWYNAWNEKRRVYEE 111
              |||||||||||||||||
Db         61 FIKWYNAWNEKRRVYEE 77
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Search completed: April 22, 2004, 12:34:55
Job time : 23 secs